GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

March 20, 2000, 05:31:20; Search time 35.25 Seconds (without alignments) 249.964 Million cell updates/sec Run on:

US-08-509-359B-138 1923 1 EELTLKYGAKHVIMLFVPVT......STDNLVRPFMDTLASHQLYI 372 Title: Perfect score: Sequence:

BLOSUM62 Scoring table: 188963 segs, 23686106 residues Searched:

A_Geneseq_36:* Database :

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Word size :

188963 Number of hits that pass the threshold : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		prese	AD4 r	prese	-uilin-	٠.	٠.	ч	٠.	AD4/AD3LP sequence	Ų,	Ψ	early on	Early onset Alzhei	Presentlin-1-1. Ne	Partial AD3 sequen	PS1/467 protein. D	PS1/429 protein. D	Human presentlin-1	Presenilin-1-1 L28	Presenilin-1-1 L39	Presenilin-1-1 V82	Presenilin-1-1 I21	Mouse PS1/467 prot	Presenilin-1-1 A28	Presenilin-1-1 A79	Presenilin-1-1 I23	Presenilin-1-1 A26	Human S182 gene pr	Presenilin-1-1 V96	Presentlin-1-1 Y11	Presenilin-1-1 114	Presenilin-1-1 A24	Human S182 gene, P		Presentlin-1-1 G38		ese	esenilin-1-1	an presenil
SUMMARIES	Al		W05762	22	96	9	92	9/	5	92	8	3	96	33	3	33	20	53	2	96	2	2	33	7	3	W05754	33	574	574	237	573	573	574	574	17	575	575	573	574	574	396
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	Score	: :	1923	25	92	91	91	191	7	172	591.	431.	431.	429.	429.	429.	429.	429.	429.	429.	426.	426.	426.	426.	426.	٠	425.	425.	425.	424.	424.	424.	424.	424.	424.	423.	423.	423.	423.	423.	423.
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Presentlin-1-1 L17	Homo sapiens PS-1. Presenilin-1-1 P26	Human presentlin I Presentlin-1-1 H16	Presenilin-1-1 G20
W05744	W56770 W05752	W42375 W05743	W05745
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467	467	463	467
74.0	73.9	73.9	73.9
1422.5	1422.5	1421.5 1420.5	1420.5
40	4 4 2 2	43	45

ALIGNMENTS

GAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWTVGMAKLDPSSQGALQ

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disease and for drug screening

'S Claim 19: Page 203-204; 238pp; English.

This polypeptide comprises human presentlin-2 (hPS2). Its amino
acid sequence was deduced from an isolated CDNA clone (see V04669).

The man and murine presentlin-1 sequences are also provided (see
W13964-66). Mutations in the PS-1 and PS-2 genes are linked to
the development in humans of forms of familial Alzheimer's disease
(FAD) and may be causative of other disorders, e.g. cognitive,
intellectual, ineurological or physiological disorders such as
cerebral haemorrhage, schizophrenia, depression, mental retardation
and epilepsy. Use of the nucleic acids and proteins comprising or
cerebral haemorrhage, schizophrenia, depression, mental retardation
and epilepsy. Use of the nucleic acids and proteins comprising or
cerebral haemorrhage and tamagenic short treatment of FAD,
and in producing cell lines and transgenic animals useful as models
condulate the activity of a presentlin protein, and methods for
identifying substances that bind to, or
identifying substances that affect the interaction of a
presentlin-interacting protein with a presentlin protein are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated mutant presentlin-1 genes - useful for developing products for use in detection, diagnosis and therapy of Alzheimer's
                                                                                                                                                                                                                                                                                'note= "Asn14111e mutation site (Claim 19)"
                                                                                                                                                                                                                                                                                                                  'note= "Met239Val mutation site (Claim 19)"
                                                                                                                                                                                                                                                                                                                                                     /note= "Ile420Thr mutation site"
                                                                                                 250. .268
/label= TM6
/note= "transmembrane domain 6"
                                'note= "transmembrane domain 5"
                                                                                                                                                                                                                                              'note= "transmembrane domain 8"
                                                                                                                                                                                                                                                                                                                                                                                                  04-JUL-1997; CA0475.
02-JAN-1997; US-034590.
05-JUL-1996; US-021703.
12-JUL-1996; US-021700.
08-NOV-1996; US-029895.
(HSCR-) HSC RES & DEV LP.
(UTOR) UNIV TORONTO GOVERNING COUNCIL.
Fraser PE, Rommens JM, St George-Hyslop PH; WPI; 98-286355/25.
                                                                                                                                         269. 387
/label TM6-7
/note= "hydrophilic loop"
388. 409
                                                245. .249
/label- TMS-6
/note= "hydrophilic loop"
                  'label = TM5
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                                                                                                                Gaps
                                                  1 EELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFTEDTPSVGQRLL 60
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  DB 1; Length 448;
                          Indels
100.0%; Score 1923; DB 1;
100.0%; Pred. No. 1.6e-200;
iive 0; Mismatches 0;
Query Match 100.
Best Local Similarity 100.
Matches 372; Conservative
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121 VAMDYPTLLLTVWNFGAVGMVCIHWKGPLVLQQAYLIMISALMALVFIKYLPEWSAWVIL 180

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New presentiin genes - useful for diagnosis, therapy and drug

PT New presentiin genes - useful for diagnosis, therapy and drug

PT Screening of familial Alzheimer's disease, cerebral disorders, etc.

Claim 4, Page - 178pp; English.

WOS763-WOS765 represent mutated versions of the human presentlin-2

CC Of Mighly conserved integral membrane proteins with a common structural

CC of highly conserved integral membrane proteins with a common structural

CC of highly conserved integral membrane proteins with a common structural

CC of highly conserved integral membrane proteins with a common structural

CC regions. Mutations in PS genes are implicated in familial Alzheimer's

CI sease (AD) and possibly other diseases such as cerebral haemorrhage,

Schizophrenia, depression etc., so detection of mutations in the DNA

cencoding the wild type sequences can be used for diagnosis of these

CC diseases. The wild type proteins, or vectors that express them or

CC containing antisense sequences, antibodies selective for these mutant

CC forms of the proteins and modulators of PS gene expression are

Detentially useful for treatment of AD etc. Transgenic animals are useful

SE sequence 448 AA;

Sequence 448 AA;
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Presentiin-2 human; mtation.
Presentiin-2; human; mt81-1; hPS1-2; PS-2; integral membrane protein; AD;
familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300
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117 LPYDPEMEEDSYDSFGEBSYPEVFEPPLIGYPGEELEEEEERGVKLGLGDFIFYSVLVGK
                                                                                                                                       AAATGSGDWNTTLACFVAILIGLCLTLLLLAVFKKALPALPISITFGLIFYFSTDNLVRP
                                                         241 LPYDPEMEEDSYDSFGEPSYPEVFEPPLTGYPGEELEEEEERGVKLGLGDFIFYSVLVGK
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29-APR-1995; US-431048.
28-JUN-1995; US-496841.
21-JUL-1995; US-509359.
(HSCR-) HSC RES & DEV LP.
(UTOR ) UNIV TORONTO GOVERNING COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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W05763;
25-JUL-1997 (first entry)
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Best Local Similarity 99.7
Matches 371; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease, cancer and against the disease, e.g. Alzhelmer's claim 29; Fig 29; 77pp; English.

Claim 29; Fig 29; 77pp; English.

Identifying genes which cause improper chromosome segregation, screening for inhibitors of chromosome missegregation promoters was exemplified using Alzhahmer's disease. The sequences given in T87401 to T87426 can be used in the above methods. It is not clear from the figure legend, the figure and the disclosure of the specification which sequence of Fig 1 and Fig 28 is the Abd/Ab3ip or the Ab3 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying genes which cause chromosome missegregation - useful for identifying causes of and treatments for diseases, e.g. Alzheimer's
                                                               VAMDYPTLLLTVWNFGAVGMVCIHWKGPLVLQQAYLIMISALMALVFIKYLPEWSAWYLL
                                                                                                        GAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWTVGMAKLDPSSQGALQ
                                                                                                                                                                                                                                                                                                                                                                                              Full AD4/AD3LP sequence. And AD3; AD4/AD3LP sequence. AD3; AD4/AD3LP; AL2heimer's disease; chromosome; missegregation; presentilin; inhibitor; AD; trisomy 21; ss. Homo sapiens.
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Pred. No. 7.6e-199;
0; Mismatches 0; 1
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99.78;
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Best Local Similarity 99.75
Watches 371; Conservative
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16-AUG-1995; US-002448.
(HARD ) HARVARD COLLEGE.
Li J, Potter H;
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Claim 4: Page -: 178pp; English.

W05763-W05766 represent mutated versions of the human presentlin-2

protein (see W05762 for wild type sequence). The presentlins are a family

of highly conserved integral membrane proteins with a common structural

motif, common alternate splicing patterns, and common mutational hot spot

cegions. Mutations in ps genes are implicated in familial Alzheimer's

disease (AD) and possibly other diseases such as cerebral haemorrhage,

schizophrenia, depression etc., so detection of mutations in the DNA

concaining the wild type sequences can be used for diagnosis of these

diseases. The wild type proteins, or vectors that express them or

containing antisense sequences, antibodies selective for these mutant

corrections of the proteins and modulators of PS gene expression are

potentially useful for treatment of AD etc. Transgenic animals are useful

as models for drug screening. The antibodies can also be used e.g. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JUJ-1997 (first entry)
Presenilin-2 delta263-296 mutation.
Presenilin-2; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; AD; familial Alzheimer's disease; cerebral haemorrhage; schizophrenia; depression; antibody; gene expression modulator; therapy; mutein.
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                                                                                                                                                                                                                                                                                        301 AAATGSGDWNTTLACFVAILIGLCLTLLLLLAVFKKALPALPISITFGLIFYFSTDNLVRP 360
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WPI; 96-49731/49.
Wew presentlin genes - useful for diagnosis, therapy and drug
screening of familial Alzheimer's disease, cerebral disorders, etc.
GAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWTVGMAKLDPSSQGALQ
                                        GAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWTVGMAKLDPSSQGALQ
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                                                                                                                                                                                 241 LPYDPEMEEDSYDSFGEPSYPEVFEPPLIGYPGEELEEEEERGVKLGLGDFIFYSVLVGK
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/note= "site of 34 residue deletion"
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28-APR-1995; US-431048.
28-UUL-1995; US-496841.
31-UUL-1995; US-509359.
(HSCR-) HSC RES & DEV LP.
(UTOR ) UNIV TORONTO GOVERNING COUNCIL.
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                                                                                     241 LPYDPEME-----EBL----EBL---- 277
                              309 VPKNPKYNTQRAERETQDSGSGNDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSGSI
                                                                     ---EEEEERGVKLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLTLLLLAVF
                                                                                                                                                                                                                                                                                                                                 Presenilin-1; PSI gene; mouse; familial Alzheimer's disease; FAD; cerebral haemorrhage; schizophrenia; depression; epilepsy; mental retardation; diagnosis; therapy; transgenic animal. Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Claim 1)"
                                                                                                                                        334 KKALPALPISITFGLIFYFSTDNLVRPFMDTLASHQLYI 372
                                                                                                                                                          /note= "Ile439Val mutation site
                                                                                                                                                                                                                                                                                                                                                                                                                          82. .100
/label= TM1
/note= "transmembrane domain 1"
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/note= "transmembrane domain 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "transmembrane domain 8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133. 154
/label= TM2
/note= "transmembrane domain 155. 163
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/note= "transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'label= TM3
'note= "transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84. .194
|label= TM3-4
|note= "hydrophilic loop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239. .243
/label= TM5-6
/note= "hydrophilic loop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= TM1-2
/note= "hydrophilic loop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "hydrophilic loop'
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/note= "hydrophilic loop'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= TM6-7
/note= "hydrophilic loop'
                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                W23966 standard; Protein; 467
                                                                                                                                                                                                                                                                                               20-JUL-1998 (first entry)
Mouse presenilin-1 homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     label= TM2-3
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US-021673.
US-021700.
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04-JUL-1997; CAO475.
02-JAN-1997; US-03459
05-JUL-1996; US-021670
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New isolated mutant presentiin-1 genes - useful for developing products for use in detection, diagnosis and therapy of Alzheimer's disease and for drug screening

T products for use in detection, diagnosis and therapy of Alzheimer's disease and for drug screening

Disclosure; Page 199-200; J38pp; English.

This polypeptide comprises the murine presentiin-1 (PS1) homologue. Its amino acids equence was deduced from an isolated CDNA clone (see V04668). Mutations in the human PS1 and PS2 genes (see V04666-68) have been linked to the development in humans of forms of familial Alzheimer's disease (FAD). All amino acids that are mutated in analysed FAD pedigrees (see W2364) were conserved in the murine homologue. Use of the nucleic acids and proteins comprising or derived from presentlins can be made in screening and diagnosing FAD, identifying and developing therapeutics for treatment of FAD, and in producing cell lines and transgenic animals useful as models of FAD. Methods for identifying substances that bind to, or modulate the activity of a presentlin protein, and methods for identifying substances that affect the interaction of a presentlin interacting protein with a presentlin protein are also disclosed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWTVGMAKLDPSSQGALQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NSVLNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIYLGEVLKTYN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-MAY-1997 (first entry)
Human early onset Alzheimer's disease (EOAD) polypeptide.
Early onset Alzheimer's disease; EOAD: neurodegenerative disease;
diagnosis; therapy; inhibitor; antagonist; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.4%; Score 1431.5; DB 1; Length 71.2%; Pred. No. 4e-147; Live 36; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26, .29
/note= "unidentified amino acid residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 KKALPALPISITFGLIFYFSTDNLVRPFMDTLASHQLYI 372
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                                                                                                              Fraser PE, Rommens JM, St George-Hyslop PH;
WPI; 98-286355/25.
08-NOV-1996; US-028895.
(HSCR-) HSC RES & DEV LP.
(UTOR ) UNIV TORONTO GOVERNING COUNCIL.
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W11839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 71.2
hes 284; Conservative
                                                                                                                                                                                     N-PSDB; V04668
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Matches
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coding sequence for wild type human PS-2. The presenting are a family of highly conserved integral membrane proteins with a common structural motif. common alternate splicing patterns, and common mutational hot spot regions. Mutations in PS genes are implicated in familial Alzheimer's disease (AD) and possibly other diseases such as cerebral haemorrhage, schizophrenia, depression etc., so detection of mutations in the DNA encoding these sequences can be used for diagnosis of these diseases. These proteins, or vectors that express them or containing antisense sequences, antibodies selective for mutant forms of these proteins (such as W03736) and modulators of PS gene expression are potentially useful for treatment of AD etc. Transgenic animals are useful as models for drug screening. The antibodies can also be used e.g. for affinity purification
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                                                                                                                                                                                                                                                                                                                                                               NSVLNTLIMISVIVVWTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIYLGEVLKTYN 120
                                                                                                                                                                                                                                                                                                                                                                                                                            131 HSILNAAIMISVIVVWTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFIYLGEVFKTYN 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAMDYPTLLLTVWNFGAVGMVCIHWKGPLVLQQAYLIMISALMALVFIKYLPEWSAWVIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          311 KNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSSSILA 370
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                                                                                                                                                                                                                                                                                                                                              EELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFTEDTPSVGQRLL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251 AVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVMLVNNAEGDPEAQRRVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         277 -EEEEERGVKLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLTLLLLAVFKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome; missegregation;
                                                                                                                                                                                                                                                                                DB 1; Length 467;
                                                                                                                                                                                                                                                                              74.3%; Score 1429.5; DB 172.3%; Pred. No. 6.6e-147; ive 33; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       336 ALPALPISITFGLIFYFSTDNLVRPFMDTLASHQLYI 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AD3; AD4/AD3LP; Alzheimer's disease; presenilin; inhibitor; AD; trisomy 21
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"L -> V"
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/note= "H -> R"
misc_difference 186
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misc_difference 350
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191 AVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVMLVNMAEGDPEAQRRVS 250
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                                                                                                                                                                                                                                                                                                                    Identifying genes which cause chromosome missegregation - useful for identifying causes of and treatments for diseases, e.g. Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFTEDTPSVGQRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251 KNSKYNAESTERESQDIVAENDDGGFSEEWEAQRDSHLGPHRSIPESRAAVQELSSSILA
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72.3%; Pred. No. 5.4e
:ive 33; Mismatches
/label= mutation
/note= "C -> Y"
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                                                                                                                                                                                          (HARD ) HARVARD COLLEGE
Li J, Potter H;
                                                                                                                             15-AUG-1996; U13314.
16-AUG-1995; US-0024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                             Li J, Potter H;
WPI; 97-165297/15.
N-PSDB; T87402.
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Best Local Simil
Matches 287; (
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Search completed: March 20, 2000, 05:31:21 Job time: 4210 sec

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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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(without alignments)
186.879 Million cell updates/sec March 18, 2000, 19:55:31; Search time 26.47 Seconds Run on:

US-08-509-359B-138 1923 1 EELTLKYGAKHVIMLFVPVT......STDNLVRPFMDTLASHQLYI 372 Title: Perfect score: Sequence:

BLOSUM62 Scoring table: 133990 seqs, 13297546 residues Searched:

Issued_Patents_AA:* Database :

0 Word size : Number of hits that pass the threshold

/cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS9_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS9_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

0	Description		.37 Sequence 137,	38 Sequence 13	37 Sequence 137	38 Sequence 138	Sequence 29,	Sequence 2,	34 Sequence 134	Sequence 4,	11-134 Sequence 134, App	Sequence 2,	Sequence 4,	Sequence 2,	Seguence 2,	8 Sequence 18	Sequence 4,	Sequence 4,	66 Sequence 160	66 Sequence 166	Sequence 3,	A-3 Sequence 3,	4A-3 Sequence 3,	5-2 Sequence 2,	3-6 Sequence 6,	.C-1 Sequence 1,	6 Sequence 6,	-3 Sequence 3,	16-3 Sequence 3,	8 0-3	7A-7 Sequence 7,	-3 Seguence 3,	3-25 Sequence 25,	-23 Sequence 23,	
COLTANDATION OF THE PROPERTY O	ΩI	i	US-08-967-101-1	ġ	80-	-08	-08	-08	80-	-08		80-	-08	80-	· 80-	-08	-08	ė	ė		ė	ġ	ř	ė	9	ė	US-08-477-453	US-08-355-84	PCT-US95-161	34-8	336-2	38-483-0	18-808-7	18-808-1	
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COMPUTE: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-NOV-1997
CLASSIFICATION 1435
PROOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:
PILING DATE: 08/592,541 NUMBER OF SEQUENCE.

CORRESPONDENCE ADDRESS:

ADDRESSEE: TESTA, HURWITZ & THIBEAULT

STREET: High Street Tower - 125 High Street ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS: LENGTH: 448 amino acids TYPE: amino acid STREET: High Street TCITY: Boston STATE: Massachusetts COUNTRY: U.S.A. single ; MOLECULE TYPE: protein US-08-967-101-137 linear STRANDEDNESS:

Gaps ö Length 448; Indels 100.0%; Score 1923; DB 2; 100.0%; Pred. No. 2.2e-190; tive 0; Mismatches 0; Best Local Similarity 100. Matches 372; Conservative Query Match

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61 NSVLNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIYLGEVLKTYN 120 1 BELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFTEDTPSVGQRLL 60 ð g à

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61 NSVLNTLIMISVLVVYTIFLVVLYKYRCYKFIHGWLIMSSLMLFFFFYIYLGEVLKTYN 120
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                                                                                                                                                                                                                                                                                                               241 LPYDPEMEEDSYDSFGEPSYPEVFEPPLTGYPGEELEEEEERGVKLGLGDFIFYSVLVGK 300
                                                                                         61 NSVLNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIYLGEVLKTYN 120
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                                       EELILKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFTEDTPSVGQRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 29, Application US/08875972
Patent No. 5885564
GENERAL INFORMATION:
APPLICANT: Huntington Potter and Jinhue Li
TITLE OF INVENTION: ASSAY FOR IDENTIFYING GENES CAUSING
TITLE OF INVENTION: CHROMOSOME NON-DISJUNCTION
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/875,972
FILING DATE: 08-AUG-97
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Granahan Esq., Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET UNBER: HU95-03PA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/002,448
FILING DATE: 16-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (781) 861-9540 INFORMATION FOR SEQ ID NO:
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STREET TWO ME.
CITY: Lexington
TWO: Massachusetts
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361 FMDTLASHQLYI 372
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02173-4799
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US-08-875-972-29
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Pred. No. 1.7e-190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROWGENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PRO;
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
COMMESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THIBEAULT
125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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APPLICATION NUMBER: US/08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 138, Application US/08592541
Patent No. 5986054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 138:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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High Street Tower -
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STATE: Massachusetts
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
US-08-592-541-138
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CITY: BO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 -QLPYDPE-MEEDSYDSFGE---PSYPEVFEPPLTGYPG------EEL----- 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         277 -EEEEERGVKLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLTLLLLAVFKK 335
                                                                                                                                                                                             1 EELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFTEDTPSYGQRLL 60
                                                                                                                                                               Gaps
                                                                                                                                                             25;
                                                                                                                          Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08875972;
Patent No. 598564;
GENERAL INFORMATION:
APPLICANT: Huntington Potter and Jinhue Li
TITLE OF INVENTION: ASSAY FOR IDENTIFYING GENES
TITLE OF INVENTION: CHROMOSOME NON-DISJUNCTION
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
                                                                                                                    Query Match
74.3%; Score 1429.5; DB 2; Length
Best Local Similarity 72.3%; Pred. No. 2e-139;
Matches 287; Conservative 33; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,972
FILING DATE: 08-AUG-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                336 ALPALPISITFGLIFYFSTDNLVRPFMDTLASHQLYI 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Granahan Esq., Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: HU95-03PA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/002,448
FILING DATE: 16-AUG-1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
              STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-967-101-134
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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US-08-875-972-4
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191 AVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNWAEGDPEAQRRVS 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             277 -EEEEERGVKLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLTLLLLLAVFKK 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 -QLPYDPE-MEEDSYDSFGE---PSYPEVFEPPLTGYPG------EEL-----
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                                                                                                                                                                                                                                                                                                                      1 EELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFTEDTPSVGQRLL
                                                                                                                                                                                                                                                                             25;
                                                                                                                                                                                                                                Length 407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 134, Application US/08592541

Patent No. 5986054

GENERAL INFORMATION:
APPLICANT: ST. GERGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: ROMENS, JOHANNA M
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSE: TESTA, HURWITZ & THIBERAULT
                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                              74.3%; Score 1429.5; DB 2; 72.3%; Pred. No. 1.6e-139; ative 33; Mismatches 52; :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            & THIBEAULT
- 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  336 ALPALPISITFGLIFYFSTDNLVRPFMDTLASHQLYI 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: TESTA, HURWITZ
High Street Tower
TELEFAX: (781) 861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 407 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Flop...
COMPUTER: FIP.
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NAME: Pitcher, Edmund R.
                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                        ; MOLECULE TYPE: protein US-08-875-972-4
                                                                                                                        linear
                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
US-08-592-541-134
                                                                                                               TOPOLOGY:
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Best Local Simi
Matches 287;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 GAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWTVGMAKLDPSSQGAL- 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |: | |: | |: | |: | 307 KNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSSSILA 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 NSVLNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIYLGEVLKTYN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 277 -EEEEERGVKLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLTLLLLAVFKK 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFTEDTPSVGQRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 -QLPYDPE-MEEDSYDSFGE---PSYPEVFEPPLIGYPG------EEL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74.3%; Score 1429.5; DB 3; Length 463; 72.3%; Pred. No. 1.9e-139; Live 33; Mismatches 52; Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08967101
Patent No. 5840540
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL ST. GEORGE-HYSLOP, PETER H
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336 ALPALPISITFGLIFYFSTDNLVRPFMDTLASHQLYI 372
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APPLICATION NUMBER: US/08/670,964
FILING DATE: 26-JUN-1996
                                                                              CLASSIFICATION: 435
PRIOR APPLICATION 435
PRIOR APPLICATION INMERS: 60/001,142
FILING DATE: 13-JUL-1995
APPLICATION NUMBER: 60/001,501
FILING DATE: 18-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: P50358
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEFRAX: 610-270-5219
                                                                                                                                                                                                                     34,344
---- P50358
                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 72.3%
Matches 287; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
OPERATING SYSTEM:
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US-08-967-101-2
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61 NSVLNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIYLGEVLKTYN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 VAMDYPTLLLTVWNFGAVGMVCIHWKGPLVLQQAYLIMISALMALVFIKYLPEWSAWVIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 GAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWTVGMAKLDPSSQGAL- 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 -QLPYDPE-MEEDSYDSFGE---PSYPEVFEPPLTGYPG-------EEL----- 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   277 -EEEEERGVKLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLTLLLLAVFKK 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFTEDTPSVGQRLL. 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53; Indels
                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CAURENY APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 74.0%; Score 1423.5; DB 2 Best Local Similarity 72.0%; Pred. No. 8.2e-139; Matches 286; Conservative 33; Mismatches 53;
E: TESTA, HURWITZ & THIBEAULT
High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 336 ALPALPISITFGLIFYFSTDNLVRPFMDTLASHQLYI 372
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; Sequence 2, Application US/08592541

; Patent No. 5986054

; GENERAL INFORMATION:

APPLICANT: ST. GEORGE-HYSLOP, PETER
                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGIH: 467 amino acids IYPE: amino acid
                                                                       STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                  U.S.A.
                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWTVGMAKLDPSSQGALQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 NSVLNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIYLGEVLKTYN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29;
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                                                                                                                                                                                                                                              APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HIRWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-NOV-1997
                                                        336 ALPALPISITFGLIFYFSTDNLVRPFMDTLASHQLYI 372
                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
                                                                                                                                                                                           Sequence 4, Application US/08967101
Patent No. 5840540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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Best Local Similarity
Matches 274; Conserv
                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02110
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                                                                                                                                                    RESULT 15
US-08-967-101-4
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Search completed: March 18, 2000, 19:55:32 Job time: 3230 sec

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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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protein search, using sw model • OM protein

Run on:

March 18, 2000, 14:11:52; Search time 41.25 Seconds (without alignments) 425.381 Million cell updates/sec

Title: Perfect score: Sequence:

US-08-509-359B-138 1923 1 EELTLKYGAKHVIMLFVPVT.....SIDNLVRPFMDTLASHQLYI 372

BLOSUM62 Scoring table: 142080 segs, 47169319 residues Searched:

PIR_62:* Database :

0 Word size : 142080 pass the threshold Number of hits that

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	in - hi	presentlin 2 - hum	seven trans-membra		S182 protein - mou		~	presentlin I-463 -	Н	-	1,	teir	hypothetical prote	ο	sperm membrane pro		potassium transpor	mg2+ transport pro	ubiquinolcytochr	ubiquinolcytochr	sodium channel mNa	integrin-associate	sodium channel pro	serotonin receptor	sodium channel pro	hypothetical prote	NADH dehydrogenase	hypothetical prote	ubiquinolcytochr	NADH dehydrogenase	H+-transporting AT	endothelin recepto	hypothetical 33.7	-cytoc	rad3 protein - fis
SUMMAKIES		OI .	158098	A56993	139174	JC5391	I78388	JC5390	858396	563683	JC5081	JC5080	S63684	S60253	T15184	T00724	A43459	A38195	T02268	H75043	S47882	148135	A55138	S36646	CHRIMI	JC6178	A33996	T11596	T11829	S01095	T11440	S52968	S02063	S13425	D65187	S22928	\$25834
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	_	Score	1923		1802.5		1431.5	4	1429.5	4	1413.5	4	1011	926	524.5	513	274	110	104	104	103	102	101.5	100.5	99.5	99.5	66	98.5	86	86	97	25	97	76	97	96.5	ė.
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probable O-antigen cytochrome-c oxida	NADH dehydrogenase endothelin recepto	oligopeptide trans	probable membrane	glucose transport	bacteriochlorophyl
B64433 E70488	QXASM4 JQ1042	D53290	S52684	A30797	875022
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507 592	488	294	768	492	484
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N N			, , , ,	. 4	
96	95.5				

ALIGNMENTS

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RESULT
158098
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protein - human

C; Species: Homo sapiens (man)
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
C; Accession: 158098
R; Rogaev, E. I.; Sherrington, R.; Rogaeva, E.A.; Levesque, G.; Ikeda, M.; Liang, Y.; C.; Cohen, D.; Lannfelt, L.; Fraser, P.E.; Rommens, J.M.; St George-Hyslop, P.H.
Axiure 376, 775-778, 1995
A; Title: Familial Alzheimer's disease in kindreds with missense mutations in a gene of A; Reference number: 158098; MUID: 95379971
A; Accession: 158098
A; Accession: I58098
A; Accession: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-448 <RES>

A;Cross-references: GB:L44577; NID:g950347; PIDN:AAC42012.1; PID:g950348

A; Gene: E5-1 C; Superfamily: presentlin

	Ö
	Gaps
448;	
Length	Indels
3 2;	ó
100.0%; Score 1923; DB 2; Length 448; 100.0%; Pred. No. 3.5e-138;	; Mismatches 0;
.08;	0
Query Match Best Local Similarity 100.0%;	Conservative
ch 11 Sim	372;
Query Mat Best Loca	Matches

ır 60	_	L 136
DTPSVGQRL		DIPSVGORL
JLIYTPFTE		OLIYTPFTE
1 EELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFTEDTPSVGQRLL 60		77 EELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGOLIYTPFTEDTPSVGORLL 136
IVVVATIKS		IVVVATIKS
LFVPVTLCM	= = = =	LFVPVTLCM
KYGAKHVIM	= = = =	CYGAKHVIM
1 EELTL	=======================================	77 EELTE
οy		g

NSVLNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIYLGEVLKTYN 120 61

196 VAMDYPTLLLTTVWNFGAVGMVCIHWKGPLVLQQAYLIMISALMALVFIKYLPEWSAWVIL 180 137 121 셤 ö

256 셤 257 181 ò 셤

241 ö 셤

à

317

g

FMDTLASHQLYI 448 FMDTLASHQLYI 372 361 ò

437

g

RESULT 2 456993 A56993 Presentlin 2 - human presentlin 2 - human N;Alternate names: Alzheimer's disease protein 4

us-08-509-359b-138.rpr

3

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A.Molecule type: mRNA
A.Residues: 1-433 <TSUA
A.Residues: 1-433 <TSUA
A.Cross-references: DBBJ:D84427; NID:g1944353; PIDN:BAA19570.1; PID:d1020347; PID:g19
A.Experimental source: brain
C.Comment: This protein plays a role in negative regulation of apoptotic cascades dur
C.Superfamily: presentiin
F.48-66/Domain: transmembrane #status predicted <TML>
F.99-119/Domain: transmembrane #status predicted <TML>
F.130-149/Domain: transmembrane #status predicted <TMA>
F.130-149/Domain: transmembrane #status predicted <TMA>
F.1310-149/Domain: transmembrane #status predicted <TMA>
F.1310-203/Domain: transmembrane #status predicted <TMA>
F.1310-227/Domain: transmembrane #status predicted <TMA>
F.1310-327/Domain: transmembrane #status predi
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A;Accession: S58396
                          and their differential
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A;Residues: 1-467 <SHED-
A;Cross-references: EMBL:L42110; NID:9904118; PIDN:AAB46416.1; PID:9904119
A;Cross-references: EMBL:L42110; NID:9904118; PIDN:AAB46416.1; PID:9904119
FF.Vidal, R.; Ghiso, J.; Wisniewski, T.; Frangione, B.
FEBS Lett. 393, 19-23, 1996
A;Title: Alzheimer's presentlin 1 gene expression in platelets and megakaryocytes.
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D.; Brookes, A.; Sanseau,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N.Alternate names: Alzheimer's disease protein 3; protein S182
C;Species: Homo sapiens (man)
C;Date: 29-Jan-1998 #sequension 13-Feb-1998 #text_change 29-Sep-1999
C;Accession: S58396; S71401; S71402
R;Sherrington, R.; Rogaev, E.I.; Liang, Y.; Rogaeva, E.A.; Levesque, G.; Ike ero, I.; Pinessi, L.; Nee, L.; Chumakov, I.; Pollen, D.; Brookes, A.; Sansea E.; Rommens, J.M.; St George-Hyslop, P.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAMDYPTLLLTVWNFGAVGMVCIHWKGPLVLQQAYLIMISALMALVFIKYLPEWSAWVIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -EEEEERGVKLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLTLLLLAVFKK 335
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TKTYNTQAPTAHPRSDSAASDDNGGFDTTWEDHRNAQIGPINSTPESRVAVQALPSNSPP
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                                and -beta cDNAs
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     1997
Biochem. Biophys. Res. Commun. 231, 392-396, A;Title: Cloning of Xenopus presentlin-alpha A;Reference number: JC5390; MUID:97223465 A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       presentlin 1, splice form 467 - human
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Best Local Simi
Matches 286;
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C;Species: Xenopus laevis (African clawed frog)
C;Species: 04-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 29-Sep-1999
C;Accession: JC390
R;Tsujimura, A.; Yasojima, K.; Hashimoto-Gotoh, T.
                                                                                                   :| :|:
309 VPKNPKYNTQRAERETQDSGSGNDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSGSI 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 NSVLNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIYLGEVLKTYN 120
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     294
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A;Cross-references: GB:L42177; NID:g904129; PIDN:AAC42094.1; PID:g904130
C;Superfamily: presenilin
                          -QLPY----DPEMEEDSYDSFGEPSYPEVFEPPLTGYPGEELEEEEERGVKLGLGDFIFY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 GAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWTVGMAKLDPSSQGALQ
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%; Pred. No. 5.1e-101;
36; Mismatches 50;
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71.28;
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Matches 284; Conservative
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sel-12 protein - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Sep-1998
C; Accession: 560253
R; Levitan, D.; Greenwald, I.
Nature 377, 351-354, 1995
A; Title: Facilitation of lin-12-mediated signalling by sel-12, a Caenorhabditis elega A; Reference number: 560253; MUID:96032531
A; Accession: 560253
A; Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 presentlin 1, splice form 374 - human N;Alternate names: Alzheimer's disease protein 3 C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 29-Sep-1999 C;Accession: S63684 R;Sahara, N; Yahagi, Y; Takagi, H.; Kondo, T.; Okochi, M.; Usami, M.; Shirasawa, FEBS Lett. 381, 7-11, 1996 A;Title: Identification and characterization of presentlin I-467, I-463 and I-374. A;Reference number: S63683; MuID:96193001
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A; Status: preliminary; nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1-374 <SAH>
A; Cross-references: EMBL:U40380; NID:g1244639; PIDN:AAB05895.1; PID:g1244640
C; Genetics:
A; Generics:
A; Genes: GDB:PSEN1; AD3; FAD; S182; PS1
A; Cross-references: GDB:135602; OMIM:104311
A; Map position: 14q24.3.14q24.3
C; Superfamily: presentiin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                      GAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWTVGMAKLDPSSQGAL-
                                                                                                                                                   --PEMEEDSYDSFGEPSYPEVFEP----PLTGYPGEEL----
                                                                                                                                                                                                                                                                                                      - EEEEERGVKLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLTLLLLAVFKK
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81.8%; Pred. No. 2.4e-69;
tive 18; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALPALPISITFGLIFYFSTDNLVRPFMDTLASHQLYI 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Matches 193; Conserv
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Greeshiln 1 protein isoform 467 - lesser mouse lemur

C.Species 4 Microcebus murinus (lesser mouse lemur)

C.Species 8 Microcebus murinus (lesser mouse lemur)

C.Species 8 Microcebus murinus (lesser mouse lemur)

C.Species 9 Microcebus murinus (lesser mouse lemur)

C.Species 11-Jan-1997 *sequence_revision 31-Jan-1997 *text_change 29-Sep-1999

C.Accession: JG5080

R.Calcada, A.; Mestre-Frances, N.; CZech, C.; Pradier, L.; Petter, A.; Bons, N.; Bellis, Biochem. Blophys. Res. Commun. 228, 430-439, 1996

A.Title: Molecular cloning, sequencing, and brain expression of the presentlin 1 gene in A.Reference number: JG5080

A.Status: nucleic acid sequence not shown

A.Residues: 11467 < CALL

A.Residues: 11467 < CALL

A.Residues: 11467 < CALL

A.Residues: Interface acid sequence not shown

A.Residues: 11467 < CALL

A.Residues: Interface acid sequence not shown

A.Residues: 11467 < CALL

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VAMDYPTLLLTVWNFGAVGMVCIHWKGPLVLQQAYLIMISALMALVFIKYLPEWSAWVIL 180
                                                                                                                                                                                                                                                                                                                                     GAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWTVGMAKLDPSSQGAL- 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |: : :|:
307 KNTKYNAQGTEREAQASVPENDDGGFSEEWEAQRDSQLGPHRSTSVSRAAVQEISSSIPA 366
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                                      NSVLNTLIMISVIVVMTIFLVVLXKXRCYKFIHGWLIMSSLMLLFLFTYIYLGEVLKTYN 120
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                                                                                                                                                                                     VAMDYPTLLLTVWNFGAVGMVCIHWKGPLVLQQAYLIMISALMALVFIKYLPEWSAWVIL
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Particles membrane protein spe-4 - Caenorhabditis elegans
NiAlternate names: probable integral membrane protein
Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: 10-Jun-1993 #sequence_ravision 18 Nov-1994 #text_change 09-Sep-1997
Cishcession: A43459; S24632; S24633
J. Cell Biol. 119, 55-68, 1992
A:Title: Mutation of a putative sperm membrane protein in Caenorhabditis elegans prevent
A:Reference number: A43459; MUID:92407040
A:Reference number: A43459
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA; mRNA
A:Residues: 1-465 <LHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Cross-references: EMBL:214067; NID:96868; PID:96869; EMBL:214066; NID:96870; PID:96871
A:Experimental source: strain Bristol N2
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
C;Genetics:
A:Introns: 69/3; 154/3; 200/1; 224/3; 300/1; 386/1; 435/1
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211 LKKVQEKASDYSKCVLMLIMFSANEKRLTAGSNQEETNEGEESTIRRTVKQTIEYYTKRE 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         327 ETSSGSSNLSSSDSSTTVSTSDISTAEECDQKEWDDLVSNSLPNNDKRPATAADALNDGE 386
: || :| |::|| |::|| 38 VKAWLTLSCLLILEGVSAQTLHDMFSQVFDQDDNNQY----YMIVLIVVPTVVYGFG- 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 VGMVCIHWKGPLVLQQAYLIMISALMALVFIKYLPEWSAWVILGAISVYDLVAVLCPKGP 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198 LRMLVETAQERNEPIFPALIYSSAMVWTVGMAKLDPSSQG------ALQLPYDPE 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    283 GVKLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLTLLLLAVFKKALPALPI 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 IHGWLIMSSLMLLF-----TFTYIYLGEVLKTYNVAMDYPTLLL----TVWNFGA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 EVNSELSKTYFLDPSFEQTTGNILLDGFINGVGTILVLGCVSFIMLAF--VLFDFR--RI 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.2%; Score 274; DB 2; Length 465; 21.5%; Pred. No. 1.5e-13; Live 80; Mismatches 127; Indels 132;
                                                                        345 TFGLIFYFSTDNLVRPFM 362
                                                                                                                    426 MLGVVFYFLTRLLMEPFV 443
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Best Local Similarity 21.58
Matches 93; Conservative
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Search completed: March 18, 2000, 14:11:54 Job time: 491 sec

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OM protein - protein search, using sw model

March 18, 2000, 18:09:18 ; Search time 32.57 Seconds (without alignments) 341.103 Million cell updates/sec Run on:

Title: Perfect score:

US-08-509-359B-138 1923 1 EELTLKYGAKHVIMLFVPVT......STDNLVRPFMDTLASHQLYI 372 Sequence:

BLOSUM62 Scoring table: 82229 seqs, 29864866 residues Searched:

SwissProt_38:* Database :

0 Word size :

82229 Number of hits that pass the threshold : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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                                                                                                                                                                                                                                                                      SIMILARITY).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE PRESENILIN FAMILY.
                                                                                                                                                            TANAMASHI H., TABIRA T.;
"Cloning of the cDNA encoding rat presentlin-2.";
"Cloning of the cDNA encoding rat presentlin-2.";
Biochim. Blophys. Acta 1396:259-262(1998).
-!- FUNCTION: MAY PLAY A ROLE IN INTRACELLULAR SIGNALING AND GENE
EXPRESSION OR IN LINKING CHROMATIN TO THE NUCLEAR MEMBRANE. MAY
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     TAKAHASHI H., MERCKEN M., NAKAZATO Y., NOGUCHI K., MURAYAMA IMAHORI K., TAKASHIMA A.;
"Cloning of cDNA and expression of the gene encoding rat
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| -> ND (IN REF. 3).
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EMBL; D83700; BAA22832.1; -.
EMBL; BA004464; BAA20406.1; -.
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FRENTZEL S., ABDEL A.S., LUEBBERT H.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
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08877; 035546; 008947;

15-JUL-1999 (Rel. 38, Created)

15-JUL-1999 (Rel. 38, Last sequence update)

15-JUL-1999 (Rel. 38, Last annotation update)

15-JUL-1999 (Rel. 38, Rel. annotation update)

PRESENILIN 2 (PS-2).

PRESENILIN 2 (PS-2).

RATUS norvegicus (Rat).

Ratus norvegicus (Rat).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Man
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A -> V (IN REF. 2).
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f; 680ACF19 CRC32;
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MEDLINE; 97473536.
PFAM; PF01080; Presenilin;
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                                                                                                                                                                                                                                                                                                                                                                                                     SHERRINGTON R., ROGAEV E.I., LIANG Y., ROGAEVA E.A., LEVESOUE G., IKEDA M., CHI H., LIN C., LI G., HOLMAN K., TSUDA T., MAR L., FONCIN J.-F., BRUNI A.C., MONTESI M.P., SORBI S., RAINERO I., PINESSI L., NEE L., CHUMAKOV I., POLLEN D., BROOKES A., SANSEAV P., POLINSKY R.J., WASCO W., DA SILVA H.A.R., HAINES J.L., PERICAR-VANCE M.A., TANZI R.E., ROSES A.D., FRASER P.E., ROMENS J.M., ST GEORGE-HYSLOP P.H.;

"Cloning of a gene bearing missense mutations in early-onset familial
       121 VAMDYPTLLLTVWNFGAVGMVCIHWKGPLVLQQAYLIMISALMALVFIKYLPEWSAWVIL 180
                                                                                                                                     SVLVGKAAATGSGDWNTTLACFVAILIGLCLTLLLLAVFKKALPALPISITFGLIFYFST 354
                                                                                                                                               240 -QLPY----DPEMBEDSYDSFGEPSYPEVFEPPLTGYPGEELEEEEERGVKLGLGDFIFY
                                                                                                              319 QOVQHIDRNTPEGANSTVEDAAETRIQ-----TQSNLSSEDPDEERGVKLGLGDFIFY
                                                 GAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWTVGMAKLDPSSQGAL-
                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                        01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
PSENI OR PSNL1 (PS-1) (S182 PROTEIN).
                                                                                                                                                                                                                                                       467 AA.
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                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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P49769;
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                                                                                                                                                                                                                                                                                                                                                             Gaps
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"Cloning of Xenopus presentlin alpha and -beta cDNAs and their
differential expression in orgenesis and embryogenesis.";
Blochem. Blophys. Res. Commun. 231:392-396(1997).

-! FUNCTION: MAY PLAY A ROLE IN NEGATIVE REGULATION OF APOPTOTIC
CASCADES DURING OGENESIS AND EMBRYOGENESIS, AND IN
DEVELOPMENTALLY MATURED TISSUES SUCH AS BRAIN TISSUE.
                                                                                                                                                                                                                                                                                                                                                                                                  1 EELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFTEDTPSVGQRLL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                           29;
                                                                                                                                                                                                                                                                                                                  74.4%; Score 1431.5; DB 1; Length 467; 71.2%; Pred. No. 4.2e-91; Live 36; Mismatches 50; Indels 29;
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PRSESUILIN ALPHA.
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Glycoprotein.
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                                                     161
195
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281
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467 AA;
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012976;
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VARIANTS AD
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      WEDLINE: 96177673.
MEDLINE: 96177673.
CRUTS M., BACKHOVENS H., WANG S.-Y., VAN GASSEN G., THEUNS J.,
DE JONGHE C., WERNERT A., DE VOECHT J., DE WINTER G., CRAS P.,
BRUYLAND M., DATSON N., WEISSENBACH J., DEN DUNNEN J.T., MARTIN J.-J.,
HENDRIKS L., VAN BROECKHOVEN C.,
"Molecular genetic analysis of familial early-onset Alzheimer's
disease linked to chromosome 14q24.3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHERRINGTON R., ROGAEV E.I., LIANG Y., ROGAEVA E.A., LEVESQUE G., IKEDA M., CHI H., LIN C., LI G., HOLMAN K., TSUDA T., MAR L., FONCIN J.-F., BRUIN A.C., MONTESI M.P., SORBI S., RAINERO I., PINESSI L., CHUMAROV I., POLLEN D., BROOKES A.AINERO I., SANSEAU P., POLINSKY R.J., WASCO W., DA SILVA H.A.R., HAINES J.L., PERICAK-VANCE M.A., TANZI R.E., ROSES A.D., FRASER P.E., ROMESNS J.M., ST GEORGE-HYSLOP P.H.;

"Cloning of a gene bearing missense mutations in early-onset familial Alzheimer's disease.";

Nature 375:754-760(1995).
191 VAVDYITVALLIWNFGVVGMIAIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLIL 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE, 96193901.
SAHARA N., YAHAGI Y.-I., TAKAGI H., KONDO T., OKOCHI M., USAMI M., SHIRASAWA T., MORI H.;
"Identification and characterization of presentlin I-467, I-463 and
                                                                                                                                                       :| :| | :| 309 VPKNPKYSTQCTEREETQDTGTGSDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSGS
                                          181 GAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWTVGMAKLDPSSQGALQ
                                                              251 AVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAEGDPEAQ--RR
                                                                                                                               LPYDP-----EMEEDSYDSFGEPSYPEVFEPPLTGYPG-------EEL---
                                                                                                                                                                                                                   ---- EEEEERGVKLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLTLLLLAV
                                                                                                                                                                                                                                     369 ILTSEDPEERGVKLGLGDFIFYSVLVGKASATASGDMNTTIACFVAILIGLCLTLLLLAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.; AND VARIANTS AD (FORMS I-467 AND I-463).
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TSUJIMURA A., HASHIMOTO-GOTOH T.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                    CRUTS M., VAN BROECKHOVEN C.;
"Presentlin mutations in Alzheimer's disease.";
Hum. Mutat. 11:183-190(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSNI_HUMAN STANDARD; PRT; 467 AA. P49768; Q14762; Q15719; Q15720; Q1-OCT-1996 (Rel. 34, Created) 01-OCT-1996 (Rel. 38, Last annotation update) PRESENILIN 1 (PS-1) (S182 PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (FORMS I-463 AND I-374).
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PSNI_HUMAN
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ACLARK R.F., HUTTON M., FULDNER R.A., FROELICH S., KARRAN E.,
ATLBOT C., CROOK R., LENDON C., PRIHAR G., HE C., KORENBLAT K.,
ARRINEZ A., WRAGG M., BUSFIELD F., BEHRENS M.I., WIERS A., NORTON J.,
ARCOS M., MADRIGAL M., PEARSON C., LINCOLN S., BAKER M., DUFF K.,
ARCOS M., MADRIGAL L., COLLINGE J., HUMPHENS C., ASWORTH T.,
ARCOS M., MADRIGAL L., COLLINGE J., HUMPHENS C., ASWORTH T.,
ANDRIES C.A., VENTER J.C., FONSEL L., AXELMAN K., LILIUS L.,
JUHNSTON J., COMBURN R., VIITANEN M., WINBLAD B., KOSIK K., HALTIA M.,
POYHONEN M., DICKSON D., MANN D., NEARY D., SNOWDEN J., LANTOS P.,
I.ANNEEL L., ROSSOR M., ROBERTS G.W., ADAMS M.D., HARDY J., GOATE A.,
The structure of the presentlin 1 ($182) gene and identification of
structure of the presentlin 1 ($182) gene and identification of
structure of coup.";
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                                                                                         VARIANTS AD L-82; H-115; T-139; R-163; T-231; L-264; V-392 AND Y-410
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MEDILIE; 97442268.
LENDON C.L., MARTINEZ A., BEHRENS I.M., KOSIK K.S., MADRIGAL L.,
NORTON J., NEUMAN R., MYERS A., BUSFIELD F., WRAGG M., ARCOS M.,
ARANGO VIANA J.C., OSSA J., RUIZ A., GOATE A.M., LOPERA F.;
"E280A PS-1 mutation causes Alzheimer's disease but age of onset is not modified by ApoE alleles.";
Hum. Mutat. 10:186-195(1997).
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                                                                                                                                                                CAMPTON D., FLAVAN J.-M., BRICE A., HANNEQUIN D., DUBOIS B.,
MARTIN C., MOREAU V., CHARBONNIER F., DIDIERJEAN O., TARDIEU S.,
PENET C., PUEL M., PASQUIER F., LE DOZE F., BELLIS G., CALENDA A.,
HEILIG R., MARTINEZ M., MALLET J., BELLIS M., CLERGET-DARPOUX F.,
AGID Y., FREBOURG T.;
"Mutations of the presentlin I gene in families with early-onset
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Three different mutations of presentlin 1 gene in early-onset
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MEDLINE; 96024664.
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Genet. 4:2363-2372(1995).
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Neurosci. Lett. 208:195-198(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Alzheimer's disease.";
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MEDLINE; 99115106
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(See http://www.isb-sib.ch/announce/
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311 KNTKYNAQGTEREAQASVPENDDGGFSEEWEAQRDSQLGPHRSTSVSRAAVQEISSSIPA 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                  EELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFTEDTPSVGQRLL 60
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                                                                                                                                                                                                                                                                                                                               -QLPYD-----PLTGYPGEEL----
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                                                                                                                                                                                   25;
                                                                                                                                                                     Length 467;
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                                                                                                           POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
MISSING (IN ISOFORM I-463).
                                                                                                                                                                                   56; Indels
                                                                                                                                                                  Query Match 73.5%; Score 1413.5; DB 1; Best Local Similarity 71.0%; Pred. No. 7.2e-90; Matches 282; Conservative 34; Mismatches 56;
                                      Alternative splicing; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                      ALPALPISITFGLIFYFSTDNLVRPFMDTLASHQLYI 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSN_DROME STANDARD; PRT; 541 AA. 002194; 002395; 076802; 15-JUL-1999 (Rel. 38, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update)
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ities requires a license agreement (send an email to license@isb-sib.ch)
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                                                                            EMBL; Z71333; CAA95930.1; -.
                              PF01080; Presenilin; 1
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467 AA;
                                              2221
2221
2221
281
281
                                        ransmembrane;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NSVLNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLIFLFTYIYLGEVLKTYN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 VAMDYPTLLLTVWNFGAVGMYCIHWKGPLVLQQAYLIMISALMALVFIKYLPEWSAWVIL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231 IDPSS-----QGALQLP------YDPEMEEDSYDSFGEPSYPEV-FEP 266
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                                                                                                                                                                                                                                                                                                           SIMILARITY).
                                                                                           HONG C.S., KOO E.H.; "Isolation of Drosophila presentlin homolog."; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFTEDTPSVGQRLL
                                                                                                                                                                                                                                          colocalization
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74; Indels
                                                                                                                                                                                                           YE Y., FORTINI M.E.;
"Characterization of Drosophila presentlin and its colociwith with Notch during development.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ/databases.
-: SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY: BELONGS TO THE PRESENTLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISSING (IN SHORT ISOFORM), GG -> RS (IN REF. 2). 796C4FE0 CRC32;
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Pred. No. 2.9e-70;
; Mismatches 74
                                                                                                                                                                                          SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS)
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                                                SEQUENCE FROM N.A. (SHORT ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U77934; AAB61139.1; -.
EMBL; U78084; AAB53369.1; -.
EMBL; AF084184; AAC33129.1; -.
EMBL; AF084184; AAC33128.1; -.
FLYBASE; FBGT0019947; PS.
PFAM; PF01080; Presentlin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.6%; Scc
50.8%; Pre
tive 61;
NeuroReport 8:1025-1029(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59304 MW;
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                                                                          STRAIN=CANTON-S;
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266
304
507
339
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Fransmembrane.
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PSNH_ARATH
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"HOP-1, a Caenorhabditis elegans presentlin, appears to be functionally redundant with SEL-12 presentlin and to facilitate LIN-12 and GLP-1 signaling.";
Proc. Natl. Acad. Sci. U.S.A. 94:12209(1997).
                                                                                                        LGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWTVGMAKLDPSSQGAL 239
                                                                                                                                                                                                                             274
                                                                                                                                                                                                                                                                                     LNSVLNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIYLGEVLKTY 119
                                                                                                                                        NVAMDYPTLLLTVWNFGAVGMVCIHWKGPLVLQQAYLIMISALMALVFIKYLPEWSAWVI 179
                              Gaps
                                                              1 BELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQ-LIYTPFTEDTPSVGQRL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY). SIMILARITY: BELONGS TO THE PRESENILIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONNELL M., MAGGI L.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY FACILITATE LIN-12 AND GLP-1 MEDIATED RECEPTION OF
INTERCELLULAR SIGNALIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                   OLPYDPEMEEDSYDSF-----GE-----PSYPEVFEPP------LTGYPGE
                                                                                                                                                                                                                                                                          ------EEEERGVKLGLGDFIFYSVLVGKAAATGSGDWNTTLACF
                                                                                                                                                                                                                                                  272 ENTIDPR-EPISSDSNISTAFPGEASCSSEIPKRPKVKRIPQKVQIESNTTASTIQNSGV
                              62;
         DB 1; Length 461;
                            74; Indels
                                                                                                                                                                                                                                                                                                                 50.5%; Score 972; DB 1
52.8%; Pred. No. 1e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
INTEGRAL MEMBRANE PROTEIN HOP-1.
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                            53; Mismatches
                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=BRISTOL N2;
MEDLINE; 98004548.
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                  Local Simi
hes 211;
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002100;
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         Query Match
                            Matches
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63 VLNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIYLGEVLKTYNVA 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLTLLLLLAVFKKALPALPISITFGLI 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
SIMILARITY: BELONGS TO THE PRESENILIN FAMILY.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-CV. COLUMBIA;
SHINN P., BUEHLER E., DEWAR K., FENG J., KIM C., LI Y., SUN H.,
CONNAX A.B., CONWAY A.R., KURTZ D., OJI O., SHEN Y.K., TORIUMI M.,
VYSOTSKAIA V., YU G., DAVIS R.W., FEDERSPIEL N.A., THEOLOGIS A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 LDPSSQGALQLPYDPEMEEDSYDSFGEPSYPEVFEPPLTGYPGEELEEEEERG-VKLGLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 49;
                                                                                                                                                                                                                                                                                                                                                                                              Length 358;
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                                                                                                                                                                                                                                                                                                                                                                                                 Score 524.5; DB 1;
Pred. No. 3e-29;
.; Mismatches 136;
                                                                                                                                                                                                                                                                                                                         CRC32;
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15-JUL-1999 (Rel. 38, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
PRESENILIN HOMOLOG.
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                                                                                                                                                                                                                                                                                                                                                                                                 27.3%; Sco
30.5%; Pre
tive 81;
                                                                                                                                                                                                                                                                                                                            MM.
                                                          WORMPEP; CIRES.8; CEO831/.
PFAM; PF01080; Presenilin; 1.
EMBL; AF021905; AAB84394.1;
EMBL; AF000265; AAB52948.1;
WORMPEP; C18E3.8; CE08317.
                                                                                                                                                                                                                                                                                                                         39864
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Matches 117; Conservative
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358 AA;
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09wet Drachydanio 073869 cyprinus ca 09640 drocophina 095465 homo sapien 012181 fugu rubrip 034086 coccyzus er 035425 phascolosor 09229 upupa epops 092577 streptomyce 033723 antechnus 035294 rattus norv p9y829 rattus norv 093346 caenorhabdi 034279 didelphis a 034279 didelphis a 034279 didelphis a 034279 didelphis a 034428 echimys did 035561 philander o 0363696 trinomys pa 034439 echimys did 080739 arabidopsis
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Q9xt97 bos taurus
                                                                                                                           March 18, 2000, 22:07:43 ; Search time 49.26 Seconds
(without alignments)
523.595 Million cell updates/sec
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1 EELTLKYGAKHVIMLFVPVT......STDNLVRPFMDTLASHQLXI 372
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Copyright (c) 1993 - 1998 Compugen Ltd.
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031099 echimys did 037099 echimys did 034973 microtus lo 034973 microtus lo 034973 microtus lo 035075 marmosa rub 035076 microtusus r 085080 arthrobacte 034427 echimys did 034424 echimys did 034429 sminthopsis 062467 mus musculu 09xp88 sminthopsis 09xn19 ondatra zib 03518 philander m 061735 mus musculu 09xb9 phaethon le 093127 balanus amp	ALIGNMENTS		449 AA.	nce update) ation update) ; Vertebrata; Mamma	la; Pecora; Bovoidea; Bovidae;		CRC32;	ore 1896; DB 6; Length 449; dd. No. 9.9e-131; Mismatches 4; Indels 0; Gaps 0;	EELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGOLIYTPFTEDTPSVGORLL 60	13	NSVLNTLIMISVIVVMTIFLVVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIYLGEVLKTYN 120 	VAMDYPTLLITVWNFGAVGMVCIHWKGPLVLQQAYLIMISALMALVFIKYLPEWSAWVIL 180 	GAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWTVGMAKLDPSSQGALQ 240
Q34429 Q37099 Q9XNM7 Q34973 Q35075 Q35080 Q34427 Q34427 Q34427 Q34427 Q34427 Q34427 Q34427 Q34427 Q34427 Q34427 Q34427 Q34427 Q34427 Q3467 Q37878 Q9XNL9 Q Q9XNL9 Q Q9XNL9 Q Q9XNL9 Q Q9XNL9 Q	ALIGN		PRT;	Created) Last seq Last ann	Ruminantia;	RI H.;	EMBL/GenBank	Score 1896; Pred. No. 9 2; Mismatch	MIVVVATIR	4IVVVATIR	CYKYRCYKE 	IHWKGPLVI HWKGPLVI	etaqernef etaqernef
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103 103:5 103:5 102:5 102:5 102:5 102:102 102:102 101:5 101:5 100:		П	Q9XT96	1999 1999 1997 1997	Eutheria; Ce Bovinae; Bos [1]	SEQUENCE FROM N TISSUE-BRAIN; SAHARA N., SHIR	Submitted (EMBL; AF038 SEQUENCE	Query Match Best Local Similarity Matches 366; Conser	~		61 NSVLNT 38 NSVLNT		
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Best Local Similarity
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Q19737; Q22692;
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01-MAY-1999
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                                                                                                                                                                                                                                                                     243
                                                                                                                                                                                                                                                                                            286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                             VWNFGAVGMVCIHWKGPLVLQQAYLIMISALMALVFIKYLPEWSAWVILGAISVYDLVAV 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164 ALVFIKYLPEWSAWVILGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMV 223
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MADELINE; 98331525.
MARENUR; 9. DEJENERO J., VALERO R., DE JONGHE C., WOODROW S.,
HENDRIKS I., BENECKHOVEN C., GONZALEZ-DUARTE R.;
"Identification of a Drosophila presentlin homologue: evidence alternatively spliced forms.";
J. Neurogenet. 12:41-54(1998).
EMBL; AF017025, AAD01611.1; -.
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47.8%; Pred. No. 6.8e-35;
tive 29; Mismatches 41;
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Matches 133; Conserv
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SEQUENCE
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Gaps
                                                                                                                                                                                                                                                                                                                                            [1] SEQUENCE FROM N.A. SEGUENCE FROM N.A. BOWELL C.S., GEGG M.E., PALMER M.S.; "Human presentiin 1 gene encodes an alternative protein-minilin."; Submitted (AnG-1998) to the EMBL/GenBank/DDBJ databases. EMBL. AJ008005; CAAO78251. - SEQUENCE 184 AA: 21073 MW; 5C6FBAEE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 YGAKHVIMLFVPVTLCM-----IVVVATIKSVRFY----TEKNGQLIYTPF--T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDTPSVGQRLL----NSVLNTLI----MISVIVVMTIFLVVLXKYRCYKFIHGWL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFTEDTPSVGQRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Secernentea, Rhabditia, Rhabditida, oditidae, Peloderinae, Caenorhabditi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NSVLNTLIMISVIVVWTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIYLG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GARDNER A.; Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 402.5; DB 4
Pred. No. 2.1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDP_ALCOHOL_P_TRANSF; 1. 45628 MW; 07336492 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    四四
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.9%; Scor. 73.5%; Pred. No. ... 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 113.5; D
Pred. No. 0.54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Secernent
Rhabditina; Rhabditoidea; Rhabditidae;
                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z67882; CAA91804.1; -.
EMBL; Z50797; CAA91804.1; JOINED.
EMBL; Z50797; CAA90677.1; -.
EMBL; Z5782; CAA90677.1; -.
EMBL; Z5782; CAA90677.1; JOINED.
PROSITE; PS00379; CDP_ALCOHOL_P.
SEQUENCE 406 AA; 45628 MW; 07
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Neognathae; Upupiformes; Upupidae; Upupa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 DKIPFHPYF--SLKDALGFANMLLFLTTLALFSPNLLGDPENFSPANPLVTPPHIKPE-- 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------WYFLFAYAILRSIPNKLGG-----VLALAASVLVLFLMPILHMSK-QRAMT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 VVLYKYRCYKFIHGWLI----MSSLMLLFLFTYIYLGEVLKTYNVAMDYPTLLLTVWNFG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 AVGMVCIHWKGPLVLQQAYLIMISALMALVFIKYLPEWSAWVILGAISVYDLVAVLCPKG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  280 EERGVKLGLGDFIF-YSVLVGKAAATGSGDWNTTLACFVAILIGLCLTLLLLAVFKKALP 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 LCMIVVVATIKSVRFYTEKNGQLIYTPFTEDTPSVGQRLLNSVLNTLIMISVIVVMTIFL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -QLPYDPEMEEDSYDSFG------EPSY---PEVFEP--PLTGYPGEELEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 ICLVVQIAT-----GLLMATHYTADT------TLAFSSV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197 PLRMLVETAQ---ERNEP-----IFPALIYSSAMVWTVGMAKLDPSSQGAL---
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
5.6%; Score 108.5; DB 8; Length 380;
Best Local Similarity 20.8%; Pred. No. 1.2;
Matches 79; Conservative 57; Mismatches 117; Indels 127;
                                                                                                                                                                                                                     SECUENCE FROM N.A.

ESPINOSA DE LOS MONTEROS A.;

Higher-level phylogeny of Trogoniformes.";

Submitted (FBE-1997) to the EMBL/GenBank/DDBJ databases.

EMBL: U89189; AAD00684.1;

Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MURPHY L., HARRIS D.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1999 (TIEMBLrel. 10, Created)
01-MAY-1999 (TIEMBLrel. 10, Last sequence update)
01-MAY-1999 (TIEMBLrel. 10, Last annotation update)
PUTATIVE INTEGRAL MEMBRANE EXPORT PROFEIN.
                                                                                                                                                                                                                                                                                                                                                   380 AA; 42348 MW; 2500441E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              748 AA
                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339 ALPISITFGLIFYFSTDNLV 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |:| |:|:
| FRPLS---QLLFWALVANLL 334
            01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [2]
SEQUENCE FROM N.A.
STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
                                                                                                                       Upupa epops.
Mitochondrion.
                                                                               CYTOCHROME B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-A3(2)
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FERROCYTOCHROME C.
-!- COFACTOR: TWO HEMBE GROUPS (BS62 AND BS66) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN (BY SIMILARITY).
EMBL; M99462; AAB61892.1;
                                                                                                                                                                                                                                                                                                                                                                                                                            KRAJEWSKI C., DRISKELL A.C., BAVERSTOCK P.R., BRAUN M.J., "Phylogenetic relationships of the thylacine (Mammalia: Thylacinidae) among dasyuroid marsupials: evidence from cytochrome b DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 KGPLRMLVE-----TAQERNEPIFPALIYSSAMVWTVGMAKL---DPS--SQ 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             271 E------WYFLFAYAILRSIPNKLGG-----VLALLASILILLIIPLLHTA-NQR 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 SV--AHICRDVNYGWLLRNLHANGASMFFMCLFLHIGRGIYYGSY-----LYKETWN 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237 GALQLPYDPE--------MEEDSYDSFGEPSYPEVFEP--PLTGYPGEEL 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 277 EEEEERGVKLGLGDFIF-YSVLVGKAAATGSGDWNTTLACFVAILIGLCLTLLLLAVFKK 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.7%; Score 110.5; DB 8; Length 381;
21.1%; Pred. No. 0.84;
Live 54; Mismatches 115; Indels 133; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 VVLYKYRCYKFIHGWLIM-----SSLMLLFLFTYIYLGEVLKTYNVAMDYPTLLLTVWN 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 FGAVGMVCIHWKGPLVLQQAYLIMISALMALVFIKYLPEWSAWVILGAISVYDLVAVLCP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 LCMIVVVATIKSVRFYTEKNGQLIYTPFTEDTPSVGQRLLNSVLNTLIMISVIVVMTIFL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 MCLIIQILT------CLFLAMHYTSDT-------LTAFT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM: PF00033; cytochrome_b_N; 1.
Mitochondrion; Electron transport; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 IGP--TLAEWVWGGYAVDKATLTRFFAFHFILPFIVTALAIVHLLFLHETGSNNPSGINP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Metatheria; Dasyuromorphia; Dasyuridae; Phascolosorex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. R. Soc. Lond., B. Biol. Sci. 250:19-27(1992).
-!- CATALYTIC ACTIVITY: QH(2) + 2 FERRICYTOCHROME C = Q + 2
                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     381 AA; 42813 MW; C6A2674F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   380 AA.
                                                                                                                                                              381
              342 ISITFGLIFYFSTDNLVRPFMDTLASH 368
                                        288 LSQT---LFWFLVENLF--ILKWLGSH 309
                                                                                                                                                                                                        Created)
                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  336 ALPALPISITFGLIFYFSTDNLV 358
                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 21.19
Matches 81; Conservative
                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                     Phascolosorex dorsalis.
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 93096825
                                                                                                                                                                                                                                                                                                           Mitochondrion
                                                                                                                                                                                                                                                                  CYTOCHROME B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sednences.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                       135 FGAVGMVCIHWKGPLVLQQAYLIMISALMALVFIKYLPEWSAWVILGAISVYDLVAVLCP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195 KGPLRMLVE------TAQERNEPIFPALIYSSAMVWTVGMAK-----LDP 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSQGALQLPYDP------PLTGYPG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           274 EELEEEEERGVKLGLGDFIF-YSVLVGKAAATGSGDWNTTLACFVAILIGLCLTLLLLAV 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : | : | : | : | : | 268 IKPE-----WYFLFAYAILRSIPNKLGG-----VLALLASILILLIMPLLHTST 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RLLNSVLNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIYLGEVLK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                      21 LCMIVVVATIKSVRFYTEKNGQLIYTPFTEDTPSVGQRLLNSVLNTLIMISVIVVMTIFL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 LTLKYGAKH-----VIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFTEDTPSVGQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 VVGMCLCI--------MACEPVHGPLLISGLGIALAELLGLVYMKFV 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 TYNVAMDYPTLLLTVWNFGAVGMVCIHWKGPLVLQQAYLIMISALMALVFIKYL 171
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
5.5%; Score 106.5; DB 8; Length 382; milarity 20.5%; Pred. No. 1.6; Conservative 53; Mismatches 115; Indels 139
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
HUANG A.M., LEE E.H.Y.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF017437; AAB70273.1; -.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
INTEGRIN-ASSOCIATED PROTEIN FORM 4.
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Query Match
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Search completed: March 18, 2000, 22:07:45 Job time: 125 sec

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151 ValMetThrilePheLeuValValLeuTyrLysTyrArgCysTyrLysPh 167
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AF171064 Caenorhabditis elegar
U35660 Caenorhabditis elegans
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U41540 Caenorhabditis elegans
U57325 Mus musculus PS-2short
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AF017025 Drosophila melanoga
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! AC009840 Drosophila melan
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St. George-Hyslop, P.H., Rommens, J.M. and Fraser, P.E.

Nucleic acids encocing presentith II

Patent: US 5840540-A 136 24-NOV-1998;

Location/Qualifiers
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1 (bases 1 to 2236)

1 Levy-Lahad, B., Wasco, W., Poorkaj, P., Romano, D. M., Oshima, J., Pettingell, W. H., Yu, C.-E., Jondro, P. D., Schmidt, S. D., Wang, K., Growley, A. C., Fu, Y. H., Guenette, S. Y., Galas, D., Nemens, E., Wijsman, E. M., Bird, T. D., Schellenberg, G. D. and Tanzi, R. E. Candidate gene for the chromosome I familial Alzheimer's disease
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Submitted (16-DEC-1997) Molecular Biology, Tokyo Institute of Psychiatry, 2-1-8 Kami-Kitazawa, Setagaya-ku, Tokyo 156, Japan Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  469 GICAIGACCAICITICICGIGGIACICIACAAGIAICGAIGCIACAAGII 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  elleHisGlyTrpLeulleMetSerSerLeuMetLeuLeuPheLeuPher 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  519 CATCCATGGCTGGTCATGTCCTCCTGATGCTCCTCTTCTTGTTCA 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TyrProThrLeuLeuLeuThrValTrpAsnPheGlyAlaValGlyMetVa 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 lCysIleHisTrpLysGlyProLeuValLeuGlnGlnAlaTyrLeuIleM 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerAlaTrpValIleLeuGlyAlaIleSerValTyrAspLeuValAlaVa 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluAsnGluGluAspGlyGluGluAspProAspArgTyrValCysSerGl
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US-08-509-359B-137 x AF038935
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98.438
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutaryota; Moderia; Sciurognathi; Muridae; Murinae; Mus.
E 1 (bases 1 to 1490)
E 2 (bases 1 to 1490)
S Sahara,N., Mori,H. and Shirasawa,T.
Unpublished
E 2 (bases 1 to 1490)
S Sahara,N., Mori,H. and Shirasawa,T.
Direct Submission
L Submitted (16-DEC-1997) Molecular Biology, Tokyo Institute of Psychiatry, 2-1-B Rami.Ritazawa, Setagaya-ku, Tokyo 156, Japan
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-DEC-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARUJO935 1490 bp mRNA ROD
Mus musculus presentlin 2 mRNA, complete cds.
AF038935
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JS AF038935
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

REFERENCE AUTHORS TITLE JOURNAL

JOURNAL

TITLE

DEFINITION

source

FEATURES

BASE COUNT

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Pharma Ltd, Preclinical

Mammalia; Eutheria; Rattus.

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83 a 557 c 570 g 478 t
                                                                                                                                                                                                   Direct Submission
Submitted (05-JUL-1996) S. Frentzel, Sandoz P
Research, PO Box, CH-4002 Basel, Switzerland
                                                   Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; 1
Rodentia; Sciuropathi; Muridae; Murinae; 1
Lobases 1 to 2088)
Frentzel,S., Abdel,A.S. and Luebbert,H.
Unpublished
2 (bases 1 to 2088)
Frentzel,S.
                                                                                                                                                                                                                                                                             1...2088
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                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
                                                                                                                                                                                                         TITLE
JOURNAL
                                                                                                              REFERENCE
AUTHORS
JOURNAL
                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                               gene
   VERSION
KEYWORDS
SOURCE
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DEFINITION R.NOTVEGICUS mRNA for presentlin-2.
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Neurobiology, Harvard Medical
Boston, MA 02115, USA
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1 (bases 1 to 1673)

1 (bases 1 to 1673)

1 in. J., Ma.J. and Potter, H.
Identification and expression analysis of a potential familiar Alzahaimer disease gene on chromosome 1 related to AD3

Proc. Natl. Acad. Sci. U.S.A. 92 (26), 12180-12184 (1995)

96109229
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="Contig WC-516, 289 ch
/chromosome="1"
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Submitted (21-AUG-1995) Jinhe Li, N
School, 220 Longwood Ave., B2-502,
Location/Qualifiers
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Alzheimer's disease.
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//translation="MITFMASDSEEPychamediate"
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                       Direct Submission
Submitted (28-MAY-1997) to the DDBJ/EMBL/GenBank databases. Hirosl
Tanahashi, National Institute of Neuroscience, Division of
Demyelinating Disease and Aging; 4-1-1 Ogawahigashi, Kodaira, Toky
187, Japan (E-mail:tanahash@ncnaxp.ncnp.go.jp, Tel:81-423-41-1717,
Fax:81-423-46-1747)
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Gaps: 0
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Tanahashi, H. and Tabira, T.
Cloning of the cDNA encoding rat
Blochim. Blophys. Acta 1396 (3),
98207716
                                                                                                                                                                                                                                                                                                                                             Sequence updated (06-Jun-1997). Sequence updated (08-Jun-1997).
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                                                                                                                                          508 CATCCATGGCTGGCTGATCATGTCCTCCTGATGCTCCTCTTGTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACGGTAGGCATGGCGAAGCTGGACCCCTCCTCTCAGGGAGCACCTGCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            spTrpAsnThrTeuAlaCysPheValAlaIleLeuIleGlyLeuCys
yGlnLeuIleTyrThrProPheThrGluAspThrProSerValGlyGlnA
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                                                                                                                                                                                                                                                                                   CCTACATCTACCTCGGGGAAGTGTTCAAGACCTACAATGTGGCCATGGAC
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                                                              rgLeuLeuAsnSerValLeuAsnThrLeuIleMetIleSerValIleVal
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561 GTCAGCTTCTATACCCGGAAGGACGGTCAGCTAATCTACACCCCATTCAC 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         761 ATCICIGIIGIIGCIGIICTITIIIICGIICATIIACTIAGGGGAAGIAI 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192 euLysThrTyrAsnValAlaMetAspTyrProThrLeuLeuLeuThrVal 208
                                                                                                                                                                                                                                                                                                                                                                                                                           109 ValArgPheTyrThrGluLysAsnGlyGlnLeulleTyrThrProPheTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 rGluAspThrProSerValGlyGlnArgLeuLeuAsnSerValLeuAsnT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .011 ATTTCAGTATATGATTTGGTGGCTGTTTTTATGTCCCAAAGGCCCACTTCG
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                                                                             261 GAGATACCIGCACCITIGICCIACITCCAGAAIGCCCAGAIGICIGAGGA
                                                                                                                    40 pGlyGluAsnThrAlaGlnTrpArgSerGlnGluAsnGluGluAspGlyG
                                                                                                                                          361 AGCAGCAGCATGACAGGCAGAGCTTGACAACCCTGAGCCAATATCTAAT
                                                                                                                                                                                                                                                                        70 GlyArgProProGly.....Le
                                                                                                                                                                                                                                                                                                            411 GGGCGCCCCAGAGTAACTCAAGACAGGTGGTGGAACAAGATGAGGAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       209 TrpAsnPheGlyAlaValGlyMetValCysIleHisTrpLysGlyProLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225 uValLeuGlnGlnAlaTyrLeuIleMetIleSerAlaLeuMetAlaLeuV
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   to: 2681
   to: A63557
   Align seg 1/1
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                                                                                                                                                                                                                                                                 986 AGCAGATGGAAGAATGAATCAGCAAGTGCAGCATATAGACAGAAACACAC 1035
                                                                                                                                                    1036 CTGAAGGTGCAAACAGCACAGTGGAGGACGCTGCAGAGACCAGGATTCAA 1085
                                                                                                                                                                                                                                                                                                                                            1265 GTTGCTGGCAGTTTTCAAGAAGCTCTCCCTGCCCTACCGATTTCTATCA 1314
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939 TACTCCTCTGCCATGATGTGGACAGTGGGAATGGCAGAT...TCCGCTAC 985
                                                                                                              321 roGluMetGluGluAspSerTyrAspSerPheGlyGluProSerTyrPro 337
                                                                                                                                                                                                                                                                                                                                                                                                                         ThrLeuAlaCysPheValAlaIleLeuIleGlyLeuCysLeuThrLeuLe 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hrPheGlyLeuIlePheTyrPheSerThrAspAsnLeuValArgProPhe 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 2681)
Talerman,A., Amson,R. and Cohen,D.
TUCLEOTIDE SEQUENCES, PROTEINS, DRUGS AND DISTREATING CANCER
PATENT: WO 9722695-A 10 26-UUN-1997;
FONDATION JEAN DAUSSET CEPH (FR)
Other publication FR 27447691 19971024
Other publication FR 2742766 19970627.
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                                       rSerGlnGlyAlaLeu.....GlnLeuProTyr....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            650
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A63557
A63557.1 GI:3717212
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709 c 658 g 650
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LOCUS A63557
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unclassified
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438

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DEFINITION ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

FEATURES COMMENT

1110

292 eulleTyrSerSerAlaMetValTrpThrValGlyMetAlaLysLeuAsp 308

US-08-509-359B-137 x A63557

alignment_block

alignment_scores:

BASE COUNT ORIGIN

human S182 gene (accession

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VSFYTRKDGQLIYLPFFEFFILGEVFKTYNVANDYVTVALLIMNFGVVGMTALHWKGF
IRLQQAYLIMISALMALVFIKYLPFWTAMLILAVISVYDLVAVLCPKGPLRMLVFTAA
ERNGTLPPALITSSTWWLVNMAGDDFBAQRVVPKNPKYNTQKARETOPGSGSGNDG
GFSEESWEAQRDSHLGPHRSTPESRAAVQELGGSILTSEDPEERGVKLGLGDFIFYSVL
VGKASATASGDWNTTIACFVAILIGLCLTLLLAIFKKALPALPISITFGLVFFATD
                                                                                                                                                                     /note="clone: composite sequence from a ~ 0.7 kb RT-PCR clone and an overlapping ~2.0 kb cDNA clone mc6-3-2 recovered from adult mouse brain cDNA library in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hevalProValThrLeuCysMetIleValValValAlaThrIleLysSer 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                294 AGCAGCAGCATGACAGGCAGAGACTTGACAACCCTGAGCCAATATCTAAT 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 GluSerProThrProArgSerCysGlnGluGlyArgGlnGlyProGluAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 GAGATACCTGCACCTTTGTCCTACTTCCAGAATGCCCAGATGTCTGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 pGlyGluAsnThrAlaGlnTrpArgSerGlnGluAsnGluGluAspGlyG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps: Gaps: Percent Identity: 64.026
                                                                                                                                                                                                                                          Bluescript at the XhoI site.
                                                                                                                                                                                                                                                                                                   188. 1591
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number L42110); putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             460
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    l. .1964
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                                                                                                                             /tissue_type="brain"
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/note="clone: compos
                                                                                                                                                                                                                                                                                                                                                                                         /function="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               σ
                                                                                      /dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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                                                                                                            /germline
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

1 (bass 1 to 1964).

Sherington, R., Rogaev, E.I., Liang, Y., Rogaeva, E.A., Levesque, G., Ikeda, M., Chi, H., Lin, C., Li, G., Holman, R., Tsuda, T., Mar, L., Poncin, J.-F., Brunni, A.C., Monctesi, M. P., Sorbl, S., Rainero, I., Pollessi, L., Nee, L., Chumakov, I., Pollen, D., Brookes, A., Sanseau, P., Pelinsky, R.J., Wasco, W., Da Silva, H.A.R., Haines, J.L., Pericak Yance, M.A., Tanal, R.E., Rosses, A.D., Fraser, P.E., Rommens, J.M. and St. George-Hyslop, P.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   familial Alzheimer's disease
Nature 375 (6534), 754-760 (1995)
95319502
On Jul 25, 1995 this sequence version replaced gi:897616.
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S182 protein.
Mus musculus (clone: 917-935) adult brain cDNA to mRNA.
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                                                                                                                                                                                                                                                                    1236 CATCGCTCCACTCCCGAGTCAAGAGCTGCTGTCCAGGAACTTTCTGGGAG 1285
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                                                                                                                                                                                             1136 ACAAAGAGGGGAGAGAGACACAGGACAGTGGTTCTGGGAACGATGATG 1185
                                                                                                                                                                                                                                   334 roSerTyrProGluValPheGluProProLeuThrGlyTyrProGly... 349
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                                                                  ProSerSerGlnGlyAlaLeuGlnLeuProTyrAspProGluMetGlu.. 324
                                                                                                                                                                                                                                                                                                                       350 ......GluGluLeu....
                                                                                                                                                      MUSSIPR 1964 bp mRNA ROD
Mus musculus S182 protein mRNA, complete cds.
L42177
Mus musculus
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VERSION
KEYWORDS
SOURCE
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AUTHORS
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2 others

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Human presentitn-1 gene exoli Early onset Alzheimer's dise Presentlin-1 exon 9. New pre
      ! Presentlin-1 exon 12. New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New presenting genes - useful for diagnosis, therapy and drug screening of familial Alzheimer's disease, cerebral disorders, etc.

Claim 8: Page 148-150; 178pp; English.

This sequence represents the coding sequence for the human presentiin-2.

This sequence represent the coding sequence for the two different of the forms of wild type human presentiin-1 (PS-1). The form represented by 140029 results from alternate splicing of the genomic DNA sequence.

T40030 represents the coding sequence for wild type mouse PS-1. The presentlins are a family of highly conserved integral membrane proteins presentlins are a family of highly conserved integral membrane proteins of the form mutational hot spot regions. Mutations in PS genes are implicated in familial Alzheimer's disease (AD) and possibly other diseases such as cerebral haemorrhage, schizophrenia, depression etc., so detection of mutations in these sequences can be used for diagnosis of these diseases. The encoded proteins, or vectors that express them or containing proteins (such as W03736) and modulators of PS gene expression are potentially useful for treatment of AD etc. Transgenic animals are useful as models for drug screening. The antibodies can also be used e.g. for sequence of a fifting purification and in immunoassays.
                                                                                                                                                                                                                                                                                                                   25-JUL-1997 (first entry)
Human presentlin-2 wild type coding sequence.
Presentlin-2; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; AD; familial Alzheimer's disease; cerebral haemorrhage; schizophrenia; depression; antibody; gene expression modulator; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ë
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28-JUN-1995; US-496841.
31-JUL-1995; US-50939.
(UTOR ) UNIV TORONTO GOVERNING COUNCIL.
Fraser PE, Rommens JM, St George-Hyslop PH; PP-PSDB; W057631/49.
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-DB=N_Geneseq_36 -QFMT=fastap -SUFFIX=rng -GAPOP-12.000
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                                                                                                               1 MetLeuThrPheMetAlaSerAspSerGluGluGluValCysAspGluAr
                                                                                                                                             gThrSerLeuMetSerAlaGluSerProThrProArgSerCysGlnGluG
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  ø
                                           Length: 448
Gaps: 0
Identity: 100.000
provides
               ΰ
                645
specific for the mutant gene,
                                                                                                to: 2236
               ວີ
               584
                                                            Percent
       diagnosing Alzheimer's disease.
Sequence 2236 BP; 488 A;
                                                                                                 from: 1
                                           Quality: 2336.00
Ratio: 5.214
Percent Similarity: 100.000
                                                                                 US-08-509-359B-137 x T51253
                                                                                                to: T51253
                                      alignment_scores:
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20-JUL-1998 (first entry)
Human presentlin-2 cDNA (hPS2).
Hresentlin-1; PSI gene; human; familial Alzheimer's disease; FAD; cerebral hamorrhage; schizophrenia; depression; epilepsy; mental retardation; diagnosis; therapy; transgenic animal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutation site (Asn14111e)"
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 267
                                                                                                  251 SeralaTrpVallleLeuGlyAlaIleSerValTyrAspLeuValAlaVa
                                                                                                                                                                                                     uProTyrAspProGluMetGluGluAspSerTyrAspSerPheGlyGluP
                                                                                                                                                                                                                                CCCCTACGACCCGGAGATGGAAGAAGACTCCTATGACAGTTTTGGGGGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1618 CATCTCCATCACGTTCGGGCTCATCTTTACTTCTCCACGGACAACCTGG
                          TCCGCGTGGGTCATCCTGGGCGCCCATCTCTGTGTATGATCTCGTGGCTGT
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787
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ID V04669 standard; cDNA; 2229
AC V04669;
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1624
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101 ValValValAlaThrIleLysSerValArgPheTyrThrGluLysAsnGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease, cancer and against Claim 28; Fig 28; 77pp; English.
Claim 28; Fig 28; 77pp; English.
Identifying genes which cause improper chromosome segregation, screening for inhibitors of chromosome missegregation and processes caused by genes encoding chromosome missegregation promoters was exemplified using Alzheimer's disease. The sequences given in T87401 to T87426 can be used in the above methods. It is not clear from the figure legend, the figure and the disclosure of the specification which sequence of Fig 1 and Fig 28 is the AD4/AD312P or the AD3 sequence.
Sequence 2276 BP; 494 A; 595 C; 662 G; 525 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; W22508.
Identifying genes which cause chromosome missegregation - useful for identifying genes of and treatments for diseases, e.g. Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                             07-DEC-1997 (first entry)
Full AD4/AD3LP sequence.
AD3: AD4/AD3LP sequence.
presenilin; inhibitor; AD; trisomy 21; ss.
1616 CATCTCCATCACGTTCGGGCTCATCTTTTACTTCTCCACGGACAACCTGG 1665
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Percent Identity: 99.777
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16-AUG-1995; US-002448.
(HARD) HARVARD COLLEGE.
Li J, Potter H;
WPI; 97-165297/15.
                                                                                                                                                                                                                                           seg_name: N_Geneseg_36:T87426
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Ratio: 5.191
nilarity: 99.777
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1D T87426 standard; DNA
AC T87426
DT O7-DEC-1997 (first of terms of the terms of th
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1210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1111 TGATCAGTGCGCTCATGGCCCTAGTGTTCATCAAGTACCTCCCAGAGTGG 1160
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                                                                                                                                                                                                                                                                                                                                                                                             408 CTTCATACCCCGAAGTCTTTGAGCCTCCCTTGACTGGCTACCCAGGGGAG 1457
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                                                     134
                                                                                                                                  134 rqLeuLeuAsnSerValLeuAsnThrLeuIleMetIleSerValIleVal 150
                                                                                                                                                                                                                ValMetThrIlePheLeuValValLeuTyrLysTyrArgCysTyrLysPh 167
                                                                                                                                                                                                                                                                                                                                                                        184 hrTyrIleTyrLeuGlyGluValLeuLysThrTyrAsnValAlaMetAsp 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       367 ellePheTyrSerValLeuValGlyLysAlaAlaAlaThrGlySerGlyA 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    384 spTrpAsnThrThrLeuAlaCysPheValAlaIleLeuIleGlyLeuCys 400
                                                                                                                                                                                                                                                                                           etileSerAlaLeuMetAlaLeuValPheileLysTyrLeuProGluTrp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                317 uProTyrAspProGluMetGluGluAspSerTyrAspSerPheGlyGluP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            334 roSerTyrProGluValPheGluProProLeuThrGlyTyrProGlyGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1458 GAGCTGGAGGAAGAGGAGGAAAGGGGCGTGAAGCTTGGCCTCGGGGACTT
                                                       yGlnLeuIleTyrThrProPheThrGluAspThrProSerValGlyGlnA
                                                                         811 GCCTCCTCAACTCCGTGCAACACCCTCATGATGATCAGGGTCATGGTG
                                                                                                                                                                                                                                  201 TyrProThrLeuLeuLeuThrValTrpAsnPheGlyAlaValGlyMetVa
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144 GGGCGCCCCAGAGTAACTCAAGACAGGTGGTGGAACAAGATGAGGAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New presenting genes - useful for diagnosis, therapy and drug
Screening of familial Alzheimer's disease, cerebral disorders, etc.

Screening of familial Alzheimer's disease, cerebral disorders, etc.

Claim 8: Page 145-146; 178pp; English.

This sequence represents the coding sequence for the murine presentilh-1.

This sequence represent the coding sequence for the two different
corns of wild type human presentiln-1 (PS-1). The form represented by
T40029 results from alternate splicing of the genomic DNA sequence.

T40031 represents the coding sequence for wild type human PS-2. The
presentilins are a family of highly conserved integral membrane proteins
with a common structural motif, common alternate splicing patterns, and
common mutational hot spot regions. Mutations in PS genes are implicated
common mutational hot spot regions. Mutations in PS genes are implicated
common mutational hot spot regions. Mutations in PS genes are implicated
common mutations in these sequences can be used for diagnosis of these diseases.
The encoded proteins, or vectors that express them or containing
antisense sequences, antibodies selective for mutant forms of the encoded
proteins (such as W05736) and modulators of PS gene expression are
potentially useful for treatment of AD etc. Transgenic animals are useful
as models for drug screening. The antibodies can also be used e.g. for
affinity purification and in immunoassays.
                                                                                                                                                                                   23-JUL-1997 (first entry)
Murine presenilin-1 wild type coding sequence.
Murine presenilin-1 wild type coding sequence.
Presenilin-1; mouse; hPS1-1; hPS1-2; PS-2; integral membrane protein; AD;
familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
depression; antibody; gene expression modulator; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        294 AGCAGCAGCATGACAGGCAGAGACTTGACAACCCTGAGCCAATATCTAAT 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40
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Percent Identity: 64.026
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28-JUN-1995; US-496641.
31-JUL-1995; US-509359.
(HSCR-) HSC RES & DEV LP.
(UTOR ) UNIV TORONTO GOVERNING COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product- presenilin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                          Seq_documentation_block:

ID 740030 standard; DNA; 1964 BP
AT 73-JUL-1997 (first entry)
DE Murine presentlin-1 wild type
KW Presentlin-1; mouse; hPS1-1;
KW Amilial Alzheimer's disease;
KW Amilial Alzheimer's disease;
KW Amis musculus.
FR Key Location/Qual
FT Cds //*tag= a
FT (28-APR-1995; US-431048.
PR 28-APR-1995; US-49641.
PR 28-APR-1995; US-431048.
PR 28-APR-1995; US
seq_name: N_Geneseq_36:T40030
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Ratio: 3.915
nilarity: 80.300
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US-08-509-359B-137 x T40030
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1238 CATCGCTCCACTCCCGAGTCAAGAGCTGCTGTCCAGGAACTTTCTGGGAG 1287 242 275 292 euileTyrSerSerAlaMetValTrpThrValGlyMetAlaLysLeuAsp 308 543 125 rGluAspThrProSerValGlyGlnArgLeuLeuAsnSerValLeuAsnT 142 158 208 225 843 844 TCGACTGCAGCAGGCGTATCTCATTATGATCAGTGCCCTCATGGCCCTGG 893 993 275 gMetLeuValGluThrAlaGlnGluArgAsnGluProllePheProAlaL 292 443 493 109 ValArgPheTyrThrGluLysAsnGlyGlnLeuIleTyrThrProPheTh 125 593 643 175 rSerLeuMetLeuLeuPheLeuPheThrTyrIleTyrLeuGlyGluValL 192 694 ATCTCTGTTGTTGCTGTTCTTTTTTCGTTCATTTACTTAGGGGAAGTAT 743 242 alPhelleLysTyrLeuProGluTrpSerAlaTrpValIleLeuGlyAla 258 894 TATTTATCAAGTACCTCCCCGAATGGACCGCATGGCTCATCTTGGCTGTG 943 92 heValProValThrLeuCysMetIleValValValAlaThrIleLysSer 108 225 uValLeuGlnGlnAlaTyrLeuIleMetIleSerAlaLeuMetAlaLeuV 259 IleSerValTyrAspLeuValAlaValLeuCysProLysGlyProLeuAr 944 ATTICAGTATATGATGATTGGTGCTGTTTTATGTCCCAAAGGCCCACTTCG 1094 CCAGAAGCCCAA.....AGGAGGGTACCCAAGAACCCCAAGTATAACACGluAspSerTyrAspSerPheGlyGluPGluGluLeu..... 334 roSerTyrProGluValPheGluProProLeuThrGlyTyrProGly... 209 TrpAsnPheGlyAlaValGlyMetValCysIleHisTrpLysGlyProLe 75 uGluGluGluLeuThrLeuLysTyrGlyAlaLysHisValIleMetLeuP euLysThrTyrAsnValAlaMetAspTyrProThrLeuLeuLeuThrVal 309 ProSerSerGlnGlyAlaLeuGlnLeuProTyrAspProGluMetGlu..

P-PSDB; W23966

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20-JUL-1998 (first entry)
Mouse presentlin-1 cDNA.
Presentlin-1: PSI gene; mouse; familial Alzheimer's disease; FAD;
Cerebral haemorrhage; schizophrenia; depression; epilepsy;
mental retardation; diagnosis; therapy; transgenic animal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTATCTATTCCTCAACAATGGTGTGGTTGGTGAATATGGCTGAAGGAGAC 1160
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1255 GTGGCTTCAGTGAGAGTGGGAGGCCCAAAGAGACAGTCACCTGGGGCCT 1304
                                                                                                                                                                                                                                                                                                                                                                                       1305 CATCGCTCCCGAGTCAAGAGCTGCTGTCCAGGAACTTTCTGGGAG 1354
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eulleTyrSerSerAlaMetValTrpThrValGlyMetAlaLysLeuAsp 308
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                                                                                 309 ProSerSerGlnGlyAlaLeuGlnLeuProTyrAspProGluMetGlu..
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02-JAN-1997; US-034590.
05-JUL-1996; US-021673.
12-JUL-1996; US-021700.
08-NOV-1996; US-021805.
(HSCN-) HSC RES & DEV LP.
(HSCN-) WINY TORONTO GOVERNING COUNCIL.
FTASET PE, ROMMEIN JM, St George-Hyslop PH;
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1D V04668 standard; CDNA; 1964 BP

T 20-JUL-1998 (first entry)
DE Mouse presentlin-1 cDNA.

WW Presentlin-1; PS1 gene; mouse;
KW cerebral haemorrhage; Schizoph
KW mental retardation; diagnosis;
FH KW mental retardation; diagnosis;
FH KRY my musculus.

Location/Quali
FT CDS 188. 1561
FT CDS 188. 1561
FT CDS 744g= a
PN W09801549-A2.

PD 15-JAN-1998.

PR 04-JUL-1996; US-021673.

PR 05-JUL-1996; US-021673.

PR 05-JUL-1996; US-021673.

PR 05-JUL-1996; US-021673.

PR 05-JUL-1996; US-022895.

PR (HSCR-) HSC RES & DEV LP.

PA (UTON) UNIV TORONTO GOVERNING
PR (TEASER PE, ROMMENS JM, ST GEOR)

PR WPI; 98-286355/25.
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292
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This course in detection, diagnosis and therapy of Alzheimer's disease and for drug screening

This course in detection, diagnosis and therapy of Alzheimer's disease and for drug screening

Disclosure; Page 197-199; 238pp; English.

This cDNA clone for a murine presentlin-1 (PSI) homologue (see W13966). It was isolated from a mouse cDNA library using a DNA probe from the human PSI gene (see V04666). Mutations in the human PSI and PSZ genes (see V04666.08) have been linked to the cavelopment in humans of forms of familial Alzheimer's disease (FAD). All amino acids that are mutated in analysed FAD pedigrees were conserved in the murine homologue. Use of the nucleic acids and proteins comprising or derived from presentlins can be made in screening and diagnosing FAD, identifying and developing therapeutics for treatment of FAD, and in producing cell lines and transgenic animals useful as models of FAD.

Sequence 1964 BP; 503 A; 503 C; 496 G; A60 T;
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Ratio: 3.915
Percent Similarity: 80.300
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                 501
         AGAAGATGAGGAGCTGACATTGAAATATGGCGCCAAGCATGTGATCATGC
                                  euPheValProValThrLeuCysMetIleValValValAlaThrIleLys
                                           SerValArgPheTyrThrGluLysAsnGlyGlnLeuIleTyrThrProPh
                                                                               eThrGluAspThrProSerValGlyGlnArgLeuLeuAsnSerValLeuA
                                                                                                                 snThrLeuIleMetIleSerValIleValValMetThrIlePheLeuVal
                                                                                                                                                   tSerSerLeuMetLeuLeuPheLeuPheThrTyrIleTyrLeuGlyGluV
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                                                                                                                                                                                                                                                                                                                                                                                                       uArgMetLeuValGluThrAlaGlnGluArgAsnGluProIlePheProA
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.LeuGluGluGluLeuThrLeuLysTyrGlyAlaLysHisValIleMetL
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Preparation of the presention peptide PSI/429 and its analogues - useful for diagnosis and treatment of Alzheimer's disease

PS Disclosure; Fig 2; 77pp; English.

This sequence encodes the PSI/467 presention peptide. This sequence is specifically stated as not being in the nucleic acid of the invention, which encodes the PSI/429 presention peptide PSI/429 (II): Cells transformed with the DNA are used to produce recombinant (II) and analogues, useful e.g. as immunogens for generating an immune response cagainst PSI/429. (II) is a new product of the PSI/429 (II): Cells which cause Alzheimer's disease (AD). The nucleic acids are generally cuseful as probes for detection and quantification of PSI/429, can also be used to relate the protein level using Ab as immunoassay reagents. Or buridise with probes are isolated for sequencing. Antibodies (Ab) can also be diagnosed at the protein level using Ab as immunoassay reagents. Or the PSI/429 gene used to identify epitopes and for affinity purification of the PSI/429 gene or polypeptide caids and peptides are useful as mindles are used as models for AD, e.g. for testing drugs. Regulators of the PSI/429 gene or polypeptide can be used to treat e.g. AD or diseases (Involving mitochondrial pathology, apoptosis and neurodegeneration. Typical regulators are antisense sequences, ribozymes, aptamers, con synthetic or natural compounds. (II) may also be used to target other coding sequences to particular cellular locations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS1/467 protein coding séquence.
Tresentilln peptide; PS1/429; immunogen; immune response; PS1 gentalresentiln peptide; PS1/429; immunogen; immune response; PS1/467; ss. apoptosis; PS1/467; ss.
1502 GTGCCTTACATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAGCTC 1551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           euProlleSerIleThrPheGlyLeuIlePheTyrPheSerThrAspAsn 432
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                                                                                                                                                                                                                                                                                                                                                                                                    399 uCysLeuThrLeuLeuLeuLeuAlaValPheLysLysAlaLeuProAlaL
                                                                                                             366 spPheIlePheTyrSerValLeuValGlyLysAlaAlaAlaThrGlySer
                                                                                                                                                                                   1402 ATTICATITICIACAGIGIICIGGIIGGIAAAGCCICAGCAACAGCCAGI
                                                                                                                                                                                                                                                     GlyAspTrpAsnThrThrLeuAlaCysPheValAlaIleLeuIleGlyLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      433 LeuValArgProPheMetAspThrLeuAlaSerHisGlnLeuTyrIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    624 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chisholm JC, Davis JN, Drache B; WPI; 98-042186/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 715 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
ID V17358 standard; DNA; 2764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUL-1996; US-683315
06-JUN-1996; US-659296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-DEC-1997.
03-JUN-1997; U09272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2764 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (FARB ) BAYER CORP
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15-JAN-1998.

04-JUL-1997; CA0475.

02-JAN-1997; US-034590.

05-JUL-1996; US-021700.

08-NOV-1996; US-029895.
                                                                                                                                                                                                                                                                                                                                               3.954
                                                                                                                                                                                                                                                                                                                                          Quality: 1467.00
                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-08-509-359B-137 x V04666
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/note=
             /note=
1422
        /*tag=
                                                                                                                                                                                                                                                                                                                                                Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                          mutation
 mutation
                    mutation
                                       mutation
 3' end of deletes
                                                                                                                                                                                                              o
"absence of exon 9 through splicing
variation, results in Asp-257 changing
to Ala and fusion of Ala-257 to Thr-291"
                                                                                                                                                                                                                                                                                                                                                                                w "C to A FAD mutation site (Ala246Glu)"
                                                                                                                                                                                                                                                                                   r
"T to C FAD mutation site (Metl39Thr)"
                                                                                                                                                                                                                                                                                                                                               "A to G FAD mutation site (His163Arg)"
                                                                                                                                                                                                                                                                                                                                                                                                  x
"C to T FAD mutation site (Ala260Val)"
                                                                                                                                                                                                                                                                                                                                                                                                                                        2
"C to T FAD mutation site (Ala285Val)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          aa
"C to G FAD mutation site (Leu286Val)"
                                                                                                                                                                                                                                                                ^{
m q}_{
m ^{1}} to C FAD mutation site (Tyr115His)"
                                                                                                                                                                                                                                                                                                     s
"T to C FAD mutation site (Ile143Thr)"
                                                                                                                                                                                                                                                                                                                                                                                                                           T FAD mutation site (Pro264Leu)"
                                                                                                                                                                                                                                                                                                                            to C FAD mutation site (Met146Leu)
                                                                                                                                                                                                                                                                                                                                                                  "G to A FAD mutation site (Ala231Thr)
                                                                                                                                                                                                                                             p
"G to C FAD mutation site (Val82Leu)"
                                                                                                                                                                       /*tag= n
/note= "deletion of 12 nucleotides from 3'
exon 4 by alternative splicing, del
val26-Gln-29 (not critical to PS1
                                                                                                                                                                                              function)".
                                                                                                                                                                                                                                                                                                                                                                                                                           ಭ
                                                                                                    'number= 10
                                                                                                          1204. .1377
/*tag= k
                                                                                                                                                1497. .2765
                                                                                                                                                            'number= 13
                                                                     018. .1116
                                                                                                                             378. .1496
                                                                                                                                          'number= 12
                                                                                        117. .1203
                                                                                                                       number- 11
                                                  797. .1017
/*tag= h
/*tag= e
/number= 5
587. .728
/*tag= f
                         'number= 6
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                               29. .796
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                                                               'number=
                                                                                   number=
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/note=
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/note=
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1027
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                                                                       exon
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                                                                                                           exon
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Products for use in detection, diagnosis and therapy of Alzheimer's products for use in detection, diagnosis and therapy of Alzheimer's products for use in detection, diagnosis and therapy of Alzheimer's disease and for drug screening

This cDNA clone, deposited as ATCC 97124, codes for human

This cDNA clone, deposited as ATCC 97124, codes for human

This cDNA clone, deposited as ATCC 97124, codes for human

This cDNA clone, deposited as ATCC 97124, codes for human

This cDNA clone, deposited as ATCC 97124, codes for man is a large of the ALZ for derived from been linked to the development in humans of forms of familial

Alzheimer's disease (FAD) and may be causative of other disorders,

G. contitive, intellectual, neurological or physiological

disorders such as cerebral haemorrhage, schizophrenia, depression,

mental retardation and epilepsy. Isolation of the hESI cDNA

followed genetic mapping of the AD3 region at 14024.3, construction

of a physical contig spanning the AD3 region, transcription mapping

and analysis of candidate genes, and recovery of candidate genes by

RT-PCR from brain mRNA. In this cDNA, exon 1 is spliced directly

of a construction of the mRNA transcription mapping

and analysis of the mRNA transcript. A mouse PSI homologue

(see V04668) and a human presentilin-2 sequences for hPSI (see

Typ661-71). Use of the nucleic acids and proteins comprising or

therracting proteins and transgenic animals useful as models

of FAD, identifying and developing therapeutics for treatment of FAD,

characting proteins are also provided.

Sequence 2765 BP; 713 T;
                                                                                                               /*tag= ac
/note= "C to G FAD mutation site (Leu392Val)"
1477
/*tag= ad
/*ote= "G to A FAD mutation site (Cys410Tyr)"
1563
ab
"G to C FAD mutation site (Gly384Ala)"
                                                                                                                                                                                                                                                                                                                                                                                                                      "A to G FAD mutation site (Ile439Val)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ::|||
355 AGGAGCACAACGACAGG...AGCCTTGGCCACCGTGAGCCATTATCT 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          255 GAGTTACCTGCACCGTTGTCCTACTTCCAGAATGCACAGATGTCTGAGGA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        305 CAACCACCTGAGCAATACTGTACGTAGCCAGAATGACAATAGAGAACGGC 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 GluSerProThrProArgSerCysGlnGluGlyArgGlnGlyProGluAs 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57
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Percent Identity: 65.665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fraser PE, Rommens JM, St George-Hyslop PH; PPSDB; W23964.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HSCR-) HSC RES & DEV LP.
(UTOR ) UNIV TORONTO GOVERNING COUNCIL.
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852 ATCTGGAATTTTGGTGTGGTGGAATGATTTCCATTCACTGGAAAGGTCC
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V29525;
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         purpose. Vectors containing or expressing a nucleic acid molecule, protein or antibody specific for mutant PSI can be administered to a patient to reduce the likelihood, or delay the onset, of Alzheimer's disease, e.g. anti-sense RNA expression can be used to decrease expression of the PSI peptide. Transgenic animals expressing the Alzheimer's disease protein can be used to test candidate therapeutics and to investigate the normal role of PSI. The PSI peptide may also be included in pharmaceutical compositions (vaccines) for Alzheimer's disease therapy.
Antibodies against the mutant polypeptide can also be used for this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ServalargPheTyrThrGluLysAsnGlyGlnLeuIleTyrThrProPh 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 ValTrpAsnPheGlyAlaValGlyMetValCysIleHisTrpLysGlyPr 224 :::|||||||||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               255 GAGTTACCTGCACCGTTGTCCTACTTCCAGAATGCACAGATGTCTGAGGA 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alLeuLysThrTyrAsnValAlaMetAspTyrProThrLeuLeuLeuThr 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74
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                                                                                                                                                                                                                                                                                                                                                                                                                                          24 GluSerProThrProArgSerCysGlnGluGlyArgGlnGlyProGluAs 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .LeuGluGluGluLeuThrLeuLysTyrGlyhlaLysHisVallleMetL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 pGlyGluAsnThrAlaGlnTrpArgSerGlnGluAsnGluGluAspGlyG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGAAGATGAGGAGCTGACATTGAAATATGGCGCCAAGCATGTGATCATGC
                                                                                                                                                                                                                                                                   Length: 466
Gaps: 8
Percent Identity: 65.451
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                                                                                                                                                                                          625 C;
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                                                                                                                                                                                                                                                                                                                                                                                                      to: T85332 from: 1
                                                                                                                                                                                          715 A;
                                                                                                                                                                                                                                                                 Quality: 1462.00
Ratio: 3.941
nilarity: 79.614
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                                                                                                                                                                                        2765 BP;
                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                   alignment_scores:
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                                                                                                                                                                                          Sequence
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PS-1; presentlin; presentlin-1; PSP-1; Alzheimer's disease; serine protease; neurodegeneration; predisposition; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1402 ATTTCATTTCTACAGTGTTCTGGTTGGTAAAGCCTCAGCAACAGCCAGT 1451
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                                                                                                                                                                                                                                                                                                                                                                          1202 AAGCACAGAAAGGGAGTCACAAGACACTGTTGCAGAGAATGATGATGGCG 1251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1102 CTCTCATTTACTCCTCAACAATGGTGTGGTTGGTGAATATGGCAGAAGGA 1151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1152 GACCCGGAAGCTCAAAGGAGAGTATCCAAAATTCCAAGCATAATGCAGA 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1252 GGTTCAGTGAGGAATGGGAAGCCCAGAGGGACAGTCATCTAGGGCCTCAT 1301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         laLeulleTyrSerSerAlaMetValTrpThrValGlyMetAlaLysLeu 307
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224 oLeuValLeuGlnGlnAlaTyrLeuIleMetIleSerAlaLeuMetAlaL
                                                                                                                                                                                                                           uArgMetLeuValGluThrAlaGlnGluArgAsnGluProIlePheProA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                383 GlyAspTrpAsnThrThrLeuAlaCysPheValAlaIleLeuIleGlyLe
                                1002 GIGATITCAGIATAIGATITAGIGGCIGITITIGIGICCGAAAGGICCACI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AspProSerSerGlnGlyAlaLeu.....GlnLeuProTyrAspProGl
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141
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Claim 1; Fig 1; 44Pp; English.
A full-length cDNA (T59535) of the early onset Alzheimer's disease
(EOAD) gene sequence codes for a 467-amino acid polypeptide (W11839)
Another full-length cDNA (T59536) of an EOAD splice variant gene codes for a 463-amino acid polypeptide (W11840). The 2 sequences can be used to generate primers and probes for the diagnosis of predisposition to Alzheimer's disease, esp. EOAD. They can also be used for prodn. of EOAD polypeptides in transformed host cells, and antisease sequences can be used for the treatment of EOAD.
Sequence 1762 BP; 442 A; 389 C; 430 G; 478 T;
                                                                                        07-MAY-1997 (first entry)

Human early onset Alzheimer's disease (EOAD) gene.

Early onset Alzheimer's disease; EOAD; neurodegenerative disease; diagnosis; gene therapy; antisense; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              277 GGCAGGAGCACAACGACGAGCCTTGGCCACCCTGAGCCATATCT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       327 AATGGACCCCCAGGGTAACTCCCGGCAGGTGGTGGAGCAAGATGAGGA 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SERICITION SERVICE ACATAGACACCCCAAGCATGTGATCATGC 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 pGly.....GluAsnThrAlaGlnTrpArgSerGlnGluAsnGluGluA 55
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Gaps: 9
Percent Identity: 65.451
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114. .1577

174. .1577

174. .260

/tag- b

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/note- "splice varian
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                            T59535 standard; cDNA; 1762 BP T59535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-1997.
26-JUN-1996; U11064.
13-JUL-1995; US-001142.
18-JUL-1995; US-001501.
(UYSF-) UNIV SOUTH FLORIDA.
Hardy JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality: 1454.00
Ratio: 3.919
Percent Similarity: 79.614
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US-08-509-359B-137 x T59535
seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 97-118980/11.
P-PSDB; W11839.
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                                                                                                                                                                                                                                       Homo sapiens
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1227 CGCTCTACACCTGAGTCACGAGCTGCTGTCCAGGAACTTTCCAGCAGTAT 1276
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1177 GGTTCAGTGAGGAATGGGAAGCCCAGAGGGACAGTCATGGGGCCTCAT 1226
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                                                          174 tSerSerLeuMetLeuLeuPheLeuPheThrTyrIleTyrLeuGlyGluV
                                                                                                                                                                                                                                                                                                                                                                                                                                         224 oLeuValLeuGlnGlnAlaTyrLeuIleMetIleSerAlaLeuMetAlaL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1077 GACCCGGAAGCICAAAGGAGAGTAICCAAAAATICCAAGTAIAATGCAGA
SerValArgPheTyrThrGluLysAsnGlyGlnLeuIleTyrThrProPh
                snThrLeuIleMetIleSerValIleValValMetThrIlePheLeuVal
                                                                                                                                                                                                                                                                                                                 191 alLeuLysThrTyrAsnValAlaMetAspTyrProThrLeuLeuThr
                                                                                                                                                                                                                                                                                                                                                                            208 ValTrpAsnPheGlyAlaValGlyMetValCysIleHisTrpLysGlyPr
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337	337 roGluValPheGluProProLeuThrGlyTyrProGly 349	_
1171	GTGAGGAATGGGAAGCCCCAGAGGGACAGTCATCTAGGGCCTCATCGCTCT 1220	0.
350		
1221	1221 ACACCTGAGTCACGAGCTGCTGTCCAGGAACTTTCCAGCAGTATCCTCGC 1270	0
353	GluGluGluGluArgGlyValLysLeuGlyLeuGlyAspPhei 368	_
1271	1271 TGGTGAAGACCCAGAGGAAGGGGAGTAAAACTTGGATTGGGAGATTCA 1320	0.
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1321	TITICIACAGIGITCIGGITGGIAAAGCCTCAGCAACAGCCAGIGGAGAC 1370	0
385		
1371		0.
401	uThrLeuLeuLeuAlaValPheLysLysAlaLeuProAlaLeuProI 418	_
1421		0
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1471		0
435	ArgProPheMetAspThrLeuAlaSerHisGlnLeuTyrIle 448	
1531		

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466 GCAGGCAGGCCCAGAGGATGGAGAGATACTGCCCAGTGGAGAAGCCAG 515
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APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-NOV-1997
FILING DATE: 13-NOV-1997
PRIOR SPELICATION DATA:
APPLICATION NUMBER: 08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-08-509-359B-137 x US-08-967-101-136
                                                                                                                                                                                                                                                                             Sequence 136, Application US/08967101
Patent No. 5840540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: PItcher, Edmund R.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 136
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: TESTA, HURWITZ
High Street Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 2285 base pairs
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Ratio: 5.214
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
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                                                                                                                                            About: Results were produced by the GenCore software, version Copyright (c) 1993-1998 Compugen Ltd.
OM of: US-08-509-359B-137 to: Issued_Patents_NA:*
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Database sequences: 214294
Database length: 5986128
Search time (sec): 26.330000
                                                                      Date: Mar 19, 2000 11:49 AM
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Query length: 448
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Sequence
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/cgn2_6/ptodata/2/ina/5C_COMB.seq:US-08-967-101-151 + 191.00 364.16
/cgn2_6/ptodata/2/ina/5D_COMB.seq:US-08-592-541-151 + 191.00 364.16
/cgn2_6/ptodata/2/ina/5C_COMB.seq:US-08-967-101-9 + 183.00 340.50 1.
                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMENS, OCHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSE: TESTA, HURNITZ & THIBEAULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     366 ATGCTCACATTCATGGCCTCTGACAGCGAGGAAGAGTGTGTGATGAGCG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     416 GACGTCCCTAATGTCGGCCGAGAGCCCCACGCGCGCGCTCCTGCCAGGAGG 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 lyArgGlnGlyProGluAspGlyGluAsnThrAlaGlnTrpArgSerGln 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 gThrSerLeuMetSerAlaGluSerProThrProArgSerCysGlnGluG 34
                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/2/ina/5C_COMB.seq:US-08-967-101-136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATINE SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  & THIBEAULT
- 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
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Align seg 1/1

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1466 CATCTTCTACAGTGTGCTGGTGGGCAAGGCGGCTGCCACGGGCAGCGGGG 1515
.216 GAAATGAGCCCATATTCCCTGCCCTGATATACTCATCTGCCATGGTGTG 1265
                                                                                                                                                                                                                                                                                                             1416 GAGCTGGAGGAGGAGGAGGAGGGGCGTGAAGCTTGGCCTCGGGGACTT 1465
                                                                                                                                                                                                                                                                                                                                                                                                                             seg_name: /cgn2_6/ptodata/2/ina/5D_COMB.seq:US-08-875-972-28
                                                                                                                                                                                            roSerTyrProGluValPheGluProProLeuThrGlyTyrProGlyGlu
                                                                                                                                                                                                                GluLeuGluGluGluGluBluArgGlyValLysLeuGlyLeuGlyAspPh
                                                                                                                                                                                                                                                                                                                                                   ellePheTyrSerValLeuValGlyLysAlaAlaAlaThrGlySerGlyA
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                                                                                                              uProTyrAspProGluMetGluGluAspSerTyrAspSerPheGlyGluP
                                  301 ThrValGlyMetAlaLySLeuAspProSerSerGlnGlyAlaLeuGlnLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .266 ACGGTTGGCATGGCGAAGCTGGACCCCTCCTCTCAGGGTGCCCTCCAGCT
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CITY: Learington
STATE: Massachusetts
COUNTRY: USA
ZIP: 0.213-479

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/875,972
FILING DATE: 08-AUG-97
CLASSIFICATION NUMBER: US 60/002,448
FILING DATE: 16-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Granahan ESq., Patricia
REGISTRATION NUMBER: 32,227
REGISTRATION NUMBER: 32,227
REGISTRATION NUMBER: 32,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  434 alArgProPheMetAspThrLeuAlaSerHisGlnLeuTyrIle 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Huntington Potter and Jinhue Li
TITLE OF INVENTION: ASSAY FOR IDENTIFYING GENES
TITLE OF INVENTION: CHROMOSOME NON-DISJUNCTION
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS,
STREET: TWO Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: HU95-03PA TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 28, Application US/08875972
Patent No. 5985564
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (781) 861-6240
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                                                                                                                                                    84 lyAlaLysHisValIleMetLeuPheValProValThrLeuCysMetIle 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ValValValAlaThrIleLysSerValArgPheTyrThrGluLysAsnGl 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 LeuCysProLysGlyProLeuArgMetLeuValGluThrAlaGlnGluA 284
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                                                                                                                                  gThrSerLeuMetSerAlaGluSerProThrProArgSerCysGlnGluG
                                                                                                                                                                                                                                                                                                                                                                     yValProGlyArgProProGlyLeuGluGluGluLeuThrLeuLysTyrG
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                                                      1 MetLeuThrPheMetAlaSerAspSerGluGluGluValCysAspGluAr
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                  to: 2285
                  from: 1
                to: US-08-592-541-136
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134

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118 GlnLeulleTyrThrProPheThrGluAspThrProSerValGlyGlnAr 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 IleHisGlyTrpLeuIleMetSerSerLeuMetLeuLeuPheTh 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         155 CAGCTCATCTACACGCCATTCACTGAGGACACACCCTCGGTGGGCCAGCG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         255 TTATGACCATCTTCTTGGTGGTGCTCTACAAGTACCGCTGCTACAAGTTC 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 AGCGAAGCACGTGATCATGCTGTGTGTGTCTCTGTGTGCATGATCG
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN PC-DOS/MS-DOS CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,972
FILING DATE: 08-AUG-97
CLASSIFCATION: 435
PRIOR APPLICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Identity: 89.071
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                                                                                                                                                                                                                                                                        NAME: Granahan Esq., Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: HU95-03PA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
TELEFAX: (781) 861-6540
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/002,448
FILING DATE: 16-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-509-359B-137 x US-08-875-972-1
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1417 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality: 1623.50
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STRANDEDNESS:
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; LOCATION:
US-08-875-972-1
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PROTEINS RELATED
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                                                                                                                                                                                    251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                655 AAATGAGACCATATICICICCCCIGATATACICATCICCCATGGIGIGGA 704
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  yrProThrLeuLeuLeuThrValTrpAsnPheGlyAlaValGlyMetVal
                                                                                                                   GEGATCCACTGGAAGGGCCCTCTGGTGCTGGAGCAGGCCTACCTCATCAT
                                                                                                                                                                                    234 tileSerAlaLeuMetAlaLeuValPheileLysTyrLeuProGluTrpS
                                                                                                                                                                                                               eralaTrpValIleLeuGlyAlaIleSerValTyrAspLeuValAlaVal
                                                                                                                                                                                                                                                                                                                                                                            LeuCysProLysGlyProLeuArgMetLeuValGluThrAlaGlnGluAr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProTyrAspProGluMetGluGluAspSerTyrAspSerPheGlyGluPr
                                           405 ACCCCACCTCTTGCTGACTGTCTGGAACTTCGGGGCAGTGGGCATGGT
                                                                                           CysIleHisTrpLysGlyProLeuValLeuGlnGlnAlaTyrLeuIleMe
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High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND F
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
CORRESPONDENCES: 183
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
; Sequence 135, Application US/08967101
; Patent No. 5840540
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201
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192 AGCAGCAGCATGACAGGCAGAGACTTGACAACCCTGAGCCAATATCTAAT 341
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APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMENS, JOHANNA M
APPLICANT: ROMENS, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
                                          1486 CCTCCCCATCTCCATCACCTTCGGGCTCGTGTTCTACTTCGCCACGGAT 1535
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                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/2/ina/5D_COMB.seq:US-08-592-541-135
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: TESTA, HURWITZ & THIBEAULT
High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-509-359B-137 x US-08-592-541-135
                                                                                                                                                                                                                                                                                                   Sequence 135, Application US/08592541 Patent No. 5986054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 135:
SEQUENCE CHARACTERISTICS:
LENGTH: 1962 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 1468.00
Ratio: 3.915
nilarity: 80.300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U.S.A.
                                                                                                                                                                                                                                                                                seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02110
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                                                                                                                                                                                   1586 C 1586
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1092 CCAGAAGCCCAA.....AGGAGGGTACCCCAAGAACCCCAAGTATAACAC 1135
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                                                                                                                                    441
                                                                                                                                                                             92 heValProValThrLeuCysMetIleValValValAlaThrIleLysSer 108
                                                                                                                                                                                                       442 TTGTCCCCGTGACCCTCTGCATGGTCGTCGTCGCCACCACCATCAAATCA 491
                                                                                                                                                                                                                                                                        109 ValArgPheTyrThrGluLysAsnGlyGlnLeuIleTyrThrProPheTh 125
                                                                                                                                                                                                                                                                                                                                                                125 rGluAspThrProSerValGlyGlnArgLeuLeuAsnSerValLeuAsnT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 hrLeuIleMetIleSerValIleValValMetThrIlePheLeuValVal 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 rSerLeuMetLeuLeuPheLeuPheThrTyrIleTyrLeuGlyGluValL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          842 TCGACTGCAGGCGTATCTCATTATGATCAGTGCCCTCATGGCCCTGG 891
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                                                                                     892 IAITTAICAAGTACCICCCGAAIGGACCGCAIGGCTCAICTIGGCTGTG
                                                                                                                                                                                                                                                                                               542 AGAAGACACTGAGACTGTAGGCCAAAGAGCCCTGCACTCGATCCTGAATG
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70 GlyArgProProGly
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seq_documentation_block:
    Sequence 133, Application US/08592541
    Sequence 133, Application US/08592541
    Patent No. 5966054
    GENERAL INFORMATION:
    APPLICANT: ST. GEORGE-HYSLOP, PETER H
    APPLICANT: ROMENS, JOHANNA M
    APPLICANT: RASER, PAUL E
    TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
    TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
    NUMBER OF SEQUENCES: 183
    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                           1152 GACCCGGAAGCTCAAAGGAGAGTATCCAAAATTCCAAGTATAATGCAGA 1201
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302 CGCTCTACACCTGAGTCACGAGCTGCTGTCCAGGAACTTTCCAGCAGTAT 1351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             335 erTyrProGluValPheGluProProLeuThrGlyTyrProGly.....
                                                                  274 uArgMetLeuValGluThrAlaGlnGluArgAsnGluProIlePheProA
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                                                                                                                                                                                                                                                                                                                                  308 AspProSerSerGlnGlyAlaLeu.....GlnLeuProTyrAspProGl
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|SS AGGAGCACAACGACAGACGG...AGCCTTGGCCACCCTGAGCCATTATCT 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 466
Gaps: 8
Percent Identity: 65.665
                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-509-359B-137 x US-08-592-541-133
                                                                                                                                                FILING DATE:
CLASSIFICATION: 800
ATTORNEY-AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEFAN: (617) 248-7000
TELEFAN: (617) 248-7100
INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                           LENGTH: 2791 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Ratio: 3.954
Percent Similarity: 79.614
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366
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|253 GGTTCAGTGAGGAATGGGAAGGCAGAGGGACAGTCATCTAGGGCCTCAT 1302
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1303 CGCTCTACACCTGAGTCACGAGCTGCTGTCCAGGAACTTTCCAGCAGTAT 1352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1153 GACCCGGAAGCTCAAAGGAGAGTATCCAAAATTCCAAGTATAATGCAGA 1202
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                                                                                                                                                              174 tSerSerLeuMetLeuLeuPheLeuPheThrTyrIleTyrLeuGlyGluV 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                291 laLeuIleTyrSerSerAlaMetValTrpThrValGlyMetAlaLysLeu 307
                453 AGAAGATGAGGAGCTGACATTGAAATATGCGCCCAAGCATGTGATCATGC 502
                                                                                      141 snThrLeuIleMetIleSerValIleValValMetThrIlePheLeuVal 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 alLeuLysThrTyrAsnValAlaMetAspTyrProThrLeuLeuThr 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           853 ATCTGGAATTTGGGTGTGGTGGAATGATTTCCATTCACTGGAAAGGTCC 902
                                                                     euPheValProValThrLeuCysMetIleValValValAlaThrIleLys 107
                                                                                                                                          108 SerValArgPheTyrThrGluLysAsnGlyGlnLeuIleTyrThrProPh 124
                                                                                                                                                                                                                 eThrGluAspThrProSerValGlyGlnArgLeuLeuAsnSerValLeuA 141
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75 .LeuGluGluGluLeuThrLeuLysTyrGlyAlaLysHisValIleMetL
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Sequence 1. Application US/08592541
| Patent No. 5986054
| GENERAL INPORMATION:
| APPLICANT: ST. GEORGE-HYSLOP, PETER H
| APPLICANT: FRASER, PAUL E
| TILLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
| TITLE OF INVENTION: GANETIC SEQUENCES AND PROTEINS RELATED
| TITLE OF INVENTION: GANETIC SEQUENCES AND PROTEINS RELATED
| TITLE OF INVENTION: GANETIC SEQUENCES AND PROTEINS RELATED
| TITLE OF INVENTION: GANETIC SEQUENCES AND PROTEINS RELATED
| TITLE OF INVENTION: GANETIC SEQUENCES: 183
| CORRESPONDENCE: 183
| ADDRESSEE: TESTA, HURWITZ & THIBEAULT
| STREET: High Street Tower - 125 High Street
| CITY: Boston STREET MASSECHUSELTS
| COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                       399 uCysLeuThrLeuLeuLeuLeuAlaValPheLysLysAlaLeuProAlaL 416
                                                                                                                                                                   GlyAspTrpAsnThrTeuAlaCysPheValAlaIleLeuIléGlyLe 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1603 CTTGTACAGCCTTTTATGGACCAATTAGCATTCCATCAATTTATATC 1650
                                                                    1403 ATTTCATTTTCTACAGTGTTCTGGTTAAAGCCTCAGCAACAGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/2/ina/5D_COMB.seq:US-08-592-541-1
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Gaps: 8
Percent Identity: 65.451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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us-08-509-359B-137 x us-08-592-541-1
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ATTORNEY/AGENT INFORMATION:
NAME: PICCHE, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2791 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
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Percent Similarity: 79.614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores
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CACAGAAGATACCGAGACTGTGGGCCAGAGAGCCCTGCACTCAATTCTGA 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValLeuTyrLysTyrArgCysTyrLysPheIleHisGlyTrpLeuIleMe 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 GAGTTACCTGCACCGTTGTCCTACTTCCAGAATGCACAGATGTCTGAGGA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 CAACCACCTGAGCAATACTNNNNN...NNNNNNAATGACAATAGAGAAC 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   277 GGCAGGAGCACAACGACAGAGGCCTTGGCCACCCTGAGCCATTATCT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                327 AATGGACGACCCCAGGGTAACTCCCGGCAGGTGGTGGAGCAAGATGAGGA 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      euPheValProValThrLeuCysMetIleValValValAlaThrIleLys 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerValArgPheTyrThrGluLysAsnGlyGlnLeuIleTyrThrProPh 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eThrGluAspThrProSerValGlyGlnArgLeuLeuAsnSerValLeuA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         snThrLeuIleMetIleSerValIleValValMetThrIlePheLeuVal 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GITCIGIAIAAAIACAGGIGCIAIAAGGICAICCAIGCCIGGCIIAIIAI 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tSerSerLeuMetLeuLeuPheLeuPheThrTyrIleTyrLeuGlyGluV 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191 alLeuLysThrTyrAsnValAlaMetAspTyrProThrLeuLeuLeuThr 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 GluSerProThrProArgSerCysGlnGluGlyArgGlnGlyProGluAs 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 LeuGluGluGluLeuThrLeuLysTyrGlyAlaLysHisValIleMetL
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                                                                                                                                                                                                                                                                                                                                                                        Gaps: 9 Percent Identity: 65.451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: 1762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: US-08-670-964-1 from: 1
                                    34,344
3ER: P50358
                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-08-509-359B-137 x US-08-670-964-1
                                  REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEFAX: 610-270-5090
                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1762 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                          Ouality: 1454.00
Ratio: 3.919
nilarity: 79.614
                      Han, William T
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; MOLECULE TYPE: CDNA
US-08-670-964-1
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                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                       TELEX
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1177 GGTTCAGTGAGAATGGGAAGCCCAGAGGGACAGTCATCTAGGGCCTCAT 1226
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                                                                                                                                              876
                                                                                                                                                                              257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyAspTrpAsnThrTeuAlaCysPheValAlaIleLeuIleGlyLe 399
877 regrerrancearcrecereaaresacrecerecerecererer 926
                                                                                                                                                                                                                                                                                                                                                                             291 laLeuIleTyrSerSerAlaMetValTrpThrValGlyMetAlaLysLeu 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 euValPheIleLysTyrLeuProGluTrpSerAlaTrpValIleLeuGly
                                                                                                                                                                                                                                                                                                              274 uArgMetLeuValGluThrAlaGlnGluArgAsnGluProIlePheProA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1227 CGCTCTACACCTGAGTCACGAGCTGCTGTCCAGGAACTTTCCAGCAGTAT
                                                                                                             224 oLeuValLeuGlnGlnAlaTyrLeuIleMetIleSerAlaLeuMetAlaL
                                                                                                                                                                                                                                              258 AlaileSerValTyrAspLeuValAlaValLeuCysProLysGlyProLe
                                                                                                                                                                                                                                                                                                                                                                                                                                            308 AspProSerSerGlnGlyAlaLeu.....GlnLeuProTyrAspProGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            322 u...MetGluGluAspSerTyrAspSerPheGlyGlu.....ProS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               335 erTyrProGluValPheGluProProLeuThrGlyTyrProGly.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/2/ina/6_COMB.seq:US-08-670-964-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08670964 Patent No. 6010874 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        399
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1421 TACATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAGCTCTTCCAA 1470
                    1321 ITITCTACAGTGTTCTGGTTGGTAAAGCCTCAGCAACAGCCAGTGGAGAC 1370
                                                                                                             1371 TGGAACACAACCATAGCCTGTTTCGTAGCCATATTAATTGGTTTGTGCCT 1420
                                                                                                                                                       401 uThrLeuLeuLeuLeuAlaValPheLysLysAlaLeuProAlaLeuProI 418
                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/2/ina/5D_COMB.seq:US-08-670-479-24
                                                                 TrpAsnThrIhrLeuAlaCysPheValAlaIleLeuIleGlyLeuCysLe
435 ArgProPheMetAspThrLeuAlaSerHisGlnLeuTyrIle 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALUKESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Hardy, John A.
APPLICANT: Goate, Alison M.
TITLE OF INVENTION: MUTANT S182 GENES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/670,479
FILING DATE: Z6-UUN-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/001,500
FILING DATE: 18-JUL-1996
APPLICATION NUMBER: 60/001,800
FILING DATE: 02-AUG-1995
ATTORNEY/AGENT INCRMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: P50361
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g_documentation_block:
Sequence 24, Application US/08670479
Patent No. 5973133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1914 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: cDNA
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TCAGTATATGATTTAGTGGCTGTTTTGTGTCCGAAAGGTCCACTTCGTAT 1016
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|||||::::|||||||||:::||
|TCTATTGTTGCTGTTCTTTTTCATTCATTACTTGGGGGAAGTGTTTA 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 ArgPheTyrThrGluLysAsnGlyGlnLeuIleTyrThrProPheThrGl 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             919
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                                                                                                                                                                                                           226 GAGTIACCIGCACCGITGICCIACTICCAGAAIGCACAGAIGTCIGAGGA 275
                                                                                                                                                                                                                                                                        317 ACCACAACGACAGACGGAGCCTTGGCCACCTGAGCCATTATCTAATGGA 366
                                                                                                                                                                                                                                                                                                                                                                                                                                        367 CGACCCCAGGGTAACTCCCGGCAGGTGGTGGAGCAAGATGAGGAAGAAGA 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226 lLeuGlnGlnAlaTyrLeuIleMetIleSerAlaLeuMetAlaLeuValP
                                                                                                                                                                                                                                                pGlyGluAsnThrAlaGlnTrpArgSerGlnGluAsnGluGluAspGlyG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         517 AGCTTTTATACCCGGAAGGATGGCCAGCTAATCTATACCCCATTCACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 euIleMetIleSerValIleValValMetThrIlePheLeuValValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCATCATGATCAGTGTCATTGTTGTTGTCATGACTATCCTCCTGGTGGTTCTG
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                                                                                                                                                                        24 GluSerProThrProArgSerCysGlnGluGlyArgGlnGlyProGluAs
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                     Gaps: 8
Percent Identity: 65.086
                                                                                                                                 to: 1914
                                                                                                                                                                                                                                                                                                                          57 luGluAspProAspArgTyrValCysSerGlyValPro
                                                                                                                                   from: 1
                                                                          alignment_block:
US-08-509-359B-137 x US-08-670-479-24
                                                                                                                                 Align seg 1/1 to: US-08-670-479-24
                   3.916
79.741
Quality: 1449.00
                                     Percent Similarity:
                     Ratio:
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1055 TCTATTGTTGCTGTTCTTTTTTTTCATTCATTATACTTGGGGGAAGTGTTTA 1104
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                                                                                                                                                                                1305 TCAGTATATGATTTAGTGGCTGTTTTGTGTCCGAAAGGTCCACTTCGTAT 1354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1455 GAAGCTCAAAGGAGAGTATCCAAAATTCCAAGTATAATGCAGAAAGCAC 1504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1555 GTGAGGAATGGGAAGCCCAGAGGGACAGTCATCTAGGGCCTCATCGCTCT 1604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :::||||||
1605 ACACCTGAGTCACGAGCTGTCCAGGAACTTTCCAGCAGTATCCTCGC 1654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1655 TGGTGAAGACCCAGAGGAAAGGGGAGTAAAACTTGGATTGGGAGATTCA 1704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               293 leTyrSerSerAlaMetValTrpThrValGlyMetAlaLysLeuAspPro 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1505 AGAAAGGGAGTCACAAGACACTGTTGCAGAGAATGATGATGGCGGGTTCA 1554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ....GluGluGluGluGluArgGlyValLysLeuGlyLeuGlyAspPheI 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lePheTyrSerValLeuValGlyLysAlaAlaAlaThrGlySerGlyAsp 384
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                                                                                                                                                                                                                                                226 lLeuGlnGlnAlaTyrLeuIleMetIleSerAlaLeuMetAlaLeuValP 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    276 tLeuValGluThrAlaGlnGluArgAsnGluProllePheProAlaLeuI 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    310 SerSerGlnGlyAlaLeu.....GlnLeuProTyrAspProGlu...Me 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tGluGluAspSerTyrAspSerPheGlyGlu......ProSerTyrP 337
                                                                                                                                                                                                                                                                                                                                         helleLysTyrLeuProGluTrpSerAlaTrpVallleLeuGlyAlaIle 259
                                                                                                                                                                                                                                                                                                                                                                                                                              ServalTyrAspLeuvalAlavalLeuCysProLysGlyProLeuArgMe 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              418 leSerIleThrPheGlyLeuIlePheTyrPheSerThrAspAsnLeuVal 434
                                                                   ysThrTyrAsnValAlaMetAspTyrProThrLeuLeuLeuThrValTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1905 CAGCCTTTTATGGACCAATTAGCATTCCATCAATTTTATATC 1946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  337 roGluValPheGluProProLeuThrGlyTyrProGly.
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seq_name: /cgn2_6/ptodata/2/ina/5D_COMB.seq:US-08-592-541-5

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GENERAL INFORMATION:
APPLICANT: ST. GEOGE-HYSLOP, PETER H
APPLICANT: ROMENS, JOHANNA M
APPLICANT: REASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 alprovalThrLeuCysMetlleValValValAlaThrIleLysSerVal 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             555 AGCACAACGACAGACGGAGCCTTGGCCACCCTGAGCCATTATCTAATGGA 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               705 CGACCCCAGGGTAACTCCCGGCAGGTGGTGGAGCAAGATGAGGAAGAAGA 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 GluSerProThrProArgSerCysGlnGluGlyArgGlnGlyProGluAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   514 CAACCACCIGAGC.....AATACTAATGACAATAGAGAACGGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 pGlyGluAsnThrAlaGlnTrpArgSerGlnGluAsnGluGluAspGlyG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 luGluAspProAspArgTyrValCysSerGlyValPro.......Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 65.086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                  3: TESTA, HURWITZ & THIBEAULT
High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: US-08-592-541-5 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/592,54:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-509-359B-137 x US-08-592-541-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 800
ATTOREY/AGENT INFORMATION:
NAME: PItcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                    Sequence 5, Application US/08592541
Patent No. 5986054
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                      STREET: High Street TO
CIT: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
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Ratio: 3.914
Percent Similarity: 79.741
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 ArgProProGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: 11;
; MOLECULE TYPE:
US-08-592-541-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores
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                                             Patent No.
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OEE

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H33787 EST110123 Rat PC-12
AA200706 mu03f12.rl Soares
A1875963 uj53c08.yl Sugano
                                                                                                                                                                                                                                                                                                                                                                                          15 (Dases) item 705, Caracteristic, Control of the North Control of May 18, 1998 this sequence version replaced gi:3137011.

In Unpublished (1997)

On May 18, 1998 this sequence version replaced gi:3137011.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-11550

Email: Robert_Strausberg@nlh.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
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Ratima Bonaldo."
88 a 203 c 177 g 184 t lothers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="squamous cell carcinoma, poorly differentiated (4 pooled tumors, including primary and metastatic)"
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                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuThrLeuLySTyrGlyAlaLySHisVallleMetLeuPheValProVa 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 233
Gaps: 0
Percent Identity: 97.425
  263
452
315
1.5e-37
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: -400P from Gibco
  831.38
818.60
823.02
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+ 412.00
+ 409.00
+ 409.00
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Locus
                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                  AI925372
                                                                                                                                                                                                                                                                                                            human.
                       gb_est11:AA200706
gb_est36:AI875963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
  gb_est4:H33787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                            VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79
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                                                                                                                                                                                                                                                                                                         SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA237206 mx18e01.71 Sozres mous
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NA2562 yx72a04.31 Sozres melanc
AA265273 mx91c12.71 Sozres melanc
H86456 yt01b06.81 Soares retina
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NX7820 yx54h10.71 Soares mous
NX7820 yx54h10.71 Soares melanc
NZ7820 yx54h10.71 Soares melanc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW177499 PW4-CT0155-220899-001-
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AA451661 zx43f07.r1 Soares_tota
AA537185 v45603.r1 Soares mous
AA26820 vb01c10.r1 Soares mous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sugano mous
NCI_CGAP_Lu
Sugano mous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H19012 ym44b02.rl Soares infant
AA210480 m086b03.rl Beddington
AA673862 vo82h01.rl Barstead mc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA231081 mwlld11.rl Soares mous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sugano r
brain, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA260597 mx76g09.rl Soares
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gb_est11:AA231081
gb_est4:H19012
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gb_est18:AA673862
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gb_est10:AA144382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gb_est24:AI225996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI287167
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gb_est10:AA16231
gb_est5:N24576
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Percent Similarity:
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                                                                                                                                                  BASE COUNT
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Unpublished (1997)

On Dec 20, 1995 this sequence version replaced gi:1130797.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausbergenih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Prayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-GGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:

LOCUS AI811581 680 bp mRNA EST 26-AUG-1999
DEFINITION WJ39404.x1 NCI_CGAP_LU19 Homo sapiens cDNA clone IMAGE:2405191 3'
ACCESSION AI831581
VERSION AI831581. GI:5452252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eucheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 680)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP pttp://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="squamous cell carcinoma, poorly differentiated (4 pooled tumors, including primary and metastatic)"
                  lyAlaValGlyMetValCysIleHisTrpLysGlyProLeuValLeuGln 228
                                                                                            GlnAlaTyrLeuIleMetIleSerAlaLeuMetAlaLeuValPheIleLy 245
 rAsnValAlaMetAspTyrProThrLeuLeuLeuThrValTrpAsnPheG
                                                                                                                                                                 /lab_host-"DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 456.
Location/Qualifiers
1. 680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="adult"
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AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
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                                                                       212
195
                                   352
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/note-"Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled lung tumor tissue, and was then primed with a Not I pooled lung tumor tissue, and was then primed with a Not I Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of pT7T3 vector. Library went through one round of Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCTCGGTGGGCCAGCGCCTCCTCAACTCCGTGCTGAACACCCCTCATCAT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212 lyAlaValGlyMetValCysIleHisTrpLysGlyProLeuValLeuGln 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 tileSerValileValValMetThrilePheLeuValValLeuTyrLysT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 yrArgCysTyrLysPhelleHisGlyTrpLeuIleMetSerSerLeuMet 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               553 ATGATCTCGTGGCTGTGCTGTACCATAGGGCCTCTGAGAATGCTGGTA 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 STyrLeuProGlufrpSerAlaTrpValIleLeuGlyAlaIleSerValT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     279 GluthralaGlnGluArgAsnGluProIlePheProAlaLeuIleTyrSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95 lThrLeuCysMet11eValValValAlaThrIleLysSerValArgPheT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CACTCTGTGCATGATCGTGGTGGTAGCCACCATCAAGTCTGTGCGCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yrThrGluLysAsnGlyGlnLeuIleTyrThrProPheThrGluAspThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 ProSerValGlyGlnArgLeuLeuAsnSerValLeuAsnThrLeuIleMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATCAGCGTCATCGTGGTTATGACCATCTTCTTGGTGGTGCTCTACAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 LeuLeuPheLeuPheThrTyrIleTyrLeuGlyGluValLeuLysThrTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGCAGTGGCATGCTGCATCCACTGGAAGGGCCCTCTGGTGCTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  503 GTACCTCCCAGAGTGGTCCGCGTGGGTCATACTGNGCGCCATCTCTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262 yrAspLeuValAlaValLeuCysProLysGlyProLeuArgMetLeuVal
                                                                                                                                                                                                                                                                                                                            Length: 226
Gaps: 0
Percent Identity: 96.903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: AI831581 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-08-509-359B-137 x AI831581
                                                                                                                                                                                                                                                                                                                            Quality: 1118.00
Ratio: 5.059
ilarity: 97.788
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501 GATCCTACCAAAGTGGTACGCGTGGGTCATCCTGAGCGCCATATCTGTGT 550
                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
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                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuLeuPheLeuPheThrTyrIleTyrLeuGlyGluValLeuLysThrTy 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 IThrLeuCysMetIleValValAlaThrIleLysSerValArgPheT 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 CIGCIGITCCICITCACCIAIAICIACCIIGGGGAAGIGCICAAGACCIA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212 lyAlaValGlyMetValCysIleHisTrpLysGlyProLeuValLeuGln 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               401 GGGCAGTGGCATGGTGCATCCACTGGAAGGGCCCTCTGGTGCTGCAG 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245 STyrLeuProGluTrpSerAlaTrpValIleLeuGlyAlaIleSerValT 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 LeuThrLeuLysTyrGlyAlaLysHisVallleMetLeuPheValProVa 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195 rAsnValAlaMetAspTyrProThrLeuLeuLeuThrValTrpAsnPheG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229 GlnAlaTyrLeuIleMetIleSerAlaLeuMetAlaLeuValPheIleLy
                                                                                                                                                                                                                                                                                                                                                                                 Length: 199
Gaps: 0
Percent Identity: 92.462
                                                                                                                                                                                                                                                                                                                                                                               Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ::
2
              Location/Qualifiers
                                                                                                                                                                                                                                                                                             147 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: AW131752 from: 1
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US-08-509-359B-137 x AW131752
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4.796
95.980
High quality
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                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                           119
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                                   source
                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
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                FEATURES
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Indublished (1997)
On Sep 19, 1997 this sequence version replaced gi:1517341.
Contact: Robert Strausberg, Ph.D.
Tal: (301) 496-11550
Email: Robert_Strausberg@ih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Glarithion: M. Cl. CGAP Clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               //tissue_type="normal prostate"
//tissue_type="normal prostate"
//tissue_type="normal prostate; vector: pT7T3D-Pac (Pharmacia)
//note="organ: prostate; vector: strand cDNA was prepared
from normal prostate bulk tissue, and was then primed with
a Not I - oligo(dT) primer. Double-stranded cDNA was
Ilgated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library is normalized, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
155 c 138 g 143 t lothers
                                                                                                                                                                                                    no3005.51 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:1102185 3' similar to TR:G1244640 G1244640 PRESENILIN I-374. ;, mRNA sequence. AA602396
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 538)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 ProvalThrLeuCysMetlleValValValAlaThrIleLysSerValAr 110
262 yrAspLeuValAlaValLeuCysProLysGlyProLeuArgMetLeu 277
                                                          551 ATGATCTCGTCGCTTGGCTGTACCAAATGGCCTGTGTGAATGCTG 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 179
Gaps: 0
Percent Identity: 98.324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seg primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. 538
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                                                                                                                                                                                                                                                                                                                         AA602396.1 GI:2436374
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US-08-509-359B-137 x AA602396
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                                                                                                                 seq_name: gb_est17:AA602396
                                                                                                                                                                            seg_documentation_block:
LOCUS AA602396
DEFINITION no30d05.s1 NC
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                                                                                                                                                                                                                                                                                                                                                                                             human.
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DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

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Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution in Grape Cone distribution in CI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
LOCUS AW12769 555 bp mRNA EST 03-DEC-1999
DEFINITION uo66603.x1 NC1_CGAP_Mam1 Mus musculus cDNA clone IMAGE:2647516 3'
similar to qb:L42177 Mus musculus S182 protein mRNA, complete cds
(MOUSE); mRNA sequence.
ACCESSION AW212769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 555) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tunor Gene Index
Unpublished (1997)
Unpublished (1997)
On Jul 7, 1999 this sequence version replaced gi:5406916.
Other_ESTs: uo66603.y1
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert-Strausbergenih.gov
                                                                                                                                                                                                                                                                                                                                                                                                      396 eulleGlyLeuCysLeuThrLeuLeuLeuLeuAlaValPheLysLysAla 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                429 rThrAspAsnLeuValArgProPheMetAspThrLeuAlaSerHisGlnL 446
309 TCATTGGCTTGTGTCTGACCCTCCTGCTGCTTGCTGTTCAAGAAGGCG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259 IGCCCCCCCCCCCATITCCATCACGITCGGGCTCATCITITACTICIC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 CACGGACAACCTGGTGCGGCCGTTCATGGACACCCTGGCCTCCCATCAGC 160
                                                                                                            329 pSerPheGlyGluProSerTyrProGluValPheGluProProLeuThrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  413 LeuproAlaLeuproIleSerIleThrPheGlyLeuIlePheTyrPheSe
                                                                                                                                                                                                                                                           346 lyTyrProGlyGluGluLeuGluGluGluGluBluArgGlyValLysLeu
                                                                                                                                                                                                                                                                                             459 GCTACCCAGGGGAGGAGGAGGAGGAAGAGGAGGAAGGGGGCGTGAAGCTT
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High quality sequence stop: 4
Location/Qualifiers
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AUTHORS
TITLE
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Eukharia; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 707)

2 (bases 1 to 707)

3 (bases 1 to 707)

4 (bases 1 to 707)

5 (bases 1 to 707)

5 (bases 1 to 707)

5 (bases 1 to 707)

6 (bases 1 to 
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       'n
wh66e09.xl NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385736 similar to SW:PSN2_HUMAN P49810 PRESENILIN 2 ;, mRNA sequence. AI765870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 296 eralaMetValTrpThrValGlyMetAlaLysLeuAspProSerSerGln 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                313 GlyAlaLeuGlnLeuProTyrAspProGluMetGluGluAspSerTyrAs 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   found through the I.M.A.G.E. Consortium/LLNL at:
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Gaps: 0
Percent Identity: 95.161
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High quality sequence stop: 466.
Location/Qualifiers
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US-08-509-359B-137 x AI765870/rev
                                                                                                         AI765870.1 GI:5232379
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4.807
97.312
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FEATURES

Align seg 1/1

BASE COUNT

ORIGIN

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LeuGlnGlnAlaTyrLeuileMetileSer 236
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                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                     ORIGIN
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LOCUS A1276606 481 bp mRNA EST 29-JAN-1999
DEFINITION q171h07.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1877821
3' similar to SW:PSN2_HUMAN P49810 PRESENILIN 2 ;, mRNA sequence.
ACCESSION A1276606
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1 (Joses 1 to 481)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Tumor Gene Index

Unpublished (1997)

On Jan 19, 1998 this sequence version replaced gi:2285413.

Contact: Robert Strausberg'enih.gov

Fel: (301) 496-1550

Fel: (301) 496-1550
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                                                                                                                                                                                                                                                                                                                                                                                             243
                                                                                                                   253 TGATGCTGCTGTTCCTCTCACCTATATCTACCTTGGGGAAGTGCTCAAG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          452
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                                                                                                                                                                                                                                                            rLysTyrArgCysTyrLysPhelleHisGlyTrpLeulleMetSerSerL 177
                                                                                                                                                                                                                                                                                                                               euMetLeuLeuPheLeuPheThrTyrIleTyrLeuGlyGluValLeuLys 193
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                   25
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AUTHORS
TITLE
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/note="Organ: modified poly: Net organ: Note; Net organ: Net organ: Net organ: Note; Net organ: Note; Net organ: Note; Net organ: Note; Net organ: Net organ:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           352 GACCTACAATGTGGCCATGGACTACCCCACCTTTGCTGACTGTCTGGA 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 GluGluLeuThrLeuLysTyrGlyAlaLysHisValIleMetLeuPheVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 GACACCCTCGGTGGGCCAGCGCCTCCTCAACTCCGTGCTGAACACCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouality: 824.00 Length: 160
Ratio: 5.150 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
                                                                                                                                                                                                                                                      /clone="IMAGE:1877821"
/clone_lib="Soares_NhHMPu_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 481
                                                                                                                                                       /organism="Homo sapiens"
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ity sequence stop: 448.
Location/Qualifiers
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BASE COUNT ORIGIN

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//occ="Occanization of the control o
                                                                                                                                                                                                                                                                                                         1 (bases 1 to 483)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptce,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1996)
On Dec 18, 1997 this sequence version replaced gi:2339814.
On Dec 18, 1997 this sequence version replaced gi:2339814.
Contact: Marra M/Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Faxis closest@watson.wustl.edu
This close is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:930758
                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                             Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/clone_lib="Sugano mouse liver mlia"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 150
Gaps: 0
Percent Identity: 90.667
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/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
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Location/Qualifiers
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US-08-509-359B-137 x AI097783
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    ACCESSION
                                         VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                AUTHORS
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                                                                                                      /clone=IrB913"
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LOCUS A1097783 483 bp mRNA EST 20-AUG-1998
DEFINITION ue35910.yl Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1482402 5' similar to gb:L42177 Mus musculus S182 protein
mRNA, complete cds (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 roValThrLeuCysMetIleValValValAlaThrIleLysSerValArg 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 TCATGATCAGCGTCATCGTGGTTATGACCATCTTCTTGGTGGTGCTCTAC 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hrTyrAsnValalaMetAspTyrProThrLeuLeuThcValTrp.As 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PThrProSerValGlyGlnArgLeuLeuAsnSerValLeuAsnThrLeuI 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGTACCGCTGCTACAAGTTCATCCATGGCTGGTTGATCATGTCTTCACT 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     uMetLeuLeuPheLeuPheThrTyrIleTyrLeuGlyGluValLeuLysT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nPheGlyAlaValGlyMetValCysIleHisTrpLysGlyProLeuValL 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 GluLeuThrLeuLysTyrGlyAlaLysHis.ValileMetLeuPheValP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 154
Gaps: 3
Percent Identity: 96.753
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4.883
97.403
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US-08-509-359B-137 x T03796
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Ratio:
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111 108 127 158 144 161 258 177

210

194

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on:

March 20, 2000, 04:21:11; Search time 35.25 Seconds (without alignments) 301.032 Million cell updates/sec

US-08-509-359B-137
2336
1 MLTFMASDSEEEVCDERTSL.....STDNLVRPFMDTLASHQLYI 448 Title: Perfect score: Sequence:

BLOSUM62 Scoring table: 188963 segs, 23686106 residues Searched:

A_Geneseq_36:* Database :

0 Word size :

188963 Number of hits that pass the threshold : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES		Ω	762	32	W23967	9	9/	9	$\overline{}$	•	$\overline{}$	~	•	~	~			••	~	_		W05736	_	W05749	~	~	~	_	_	•	•	••			-4	5677	575	ͺ	74	575	75	
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Gaps

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Length 448; Indels

100.0%; Score 2336; DB 1; 100.0%; Pred. No. 7.3e-237; ive 0; Mismatches 0;

Local Similarity 100. nes 448; Conservative

Query Match Best Local Simi Matches 448;

9 9

1 MLTFMASDSEEEVCDERTSLMSAESPTPRSCQEGRQGPEDGENTAQWRSQENEEDGEEDP

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180 240

121 YIPFTEDTPSVGQRLANSVLNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLL

YTPFTEDTPSVGQRLLNSVLNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLL

121

FLFTYIXLGEVLKTYNVAMDYPTLLLTVWNFGAVGMYCIHWKGPLVLQQAYLIMISALMA

181

Presenilin-1-1 C26 Human early onset 840 Farly onset Alchei 734 Funan presenilin-1-2. Ne 965 Human presenilin-1 Human presenilin I	T 1 W05762 standard; Protein; 448 AA. W05762 standard; Protein; 448 AA. W05762 standard; Protein; 448 AA. W05762 standard; First entry) Presenilin-2; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; AD; femilial Alzheimer's disease; cerebral haemorrhage; schizophrenia; depression; antibody; gene expression modulator; therapy. Homo sapiens. 31-OCT-1996. 32-APR-1995; CA-03164. 28-APR-1995; US-03839. (HGCR) JUNY TORONTO GOVERNING COUNCIL. Fraser PE, Rommens JM, St George-Hyslop PH; WPTSDB; T40031. New presentin genes - useful for diagnosis, therapy and drug femilial Alzheimer's disease, cerebral disorders, etc. Claim 4; Page 146-150; 178pp; English. Nersob; T40031. New presentin genes - useful for diagnosis, therapy and drug femilial Alzheimer's diseases, cerebral disorders, etc. Claim 4; Page 146-150; 178pp; English. Nersob; T40031. Ners
W05750 W11839 W11840 W05734 W23965 W42375	n; 448 AA. IY) S1-1; hPS1-2 sease; cerebene expression WERNING COUN St George Lizheimer's clizheimer's clizheimer che geomeir clizheimer clizheim
нанан	sefu. 1-1; sease c. 2 Sefu. 3
467 463 463 463 463	(first entry) (first entry) (ilin-2. ; human; hPS1-1; hPS heimer's disease; ce antibody; gene expre. (GA0263. (US-431048. US-503359. RES & DEV LP. (TORONTO GOVERNING C FORMENS JM, St GEOI 31/49. (In genes - useful fo familial Alzheimer' e 148-150, 178pp; En e 1
622.2 622.2 622.2 620.0 61.0	standard; Pr. 1997 (first resenilin-2; human lin-2; human lon; antibod piens. 1996; CA0263 1996; CA0263 1996; CA0263 1995; US-430 110-1, (PS-1) 110-1, (P
1455 1455 1454 3 1448 1448 1446	W05762 standard; Protein; 448 AA. W05762; 25-JUL-1997 (first entry) Human presentiin-2; Presentiin-2; human; hPS1-1; hPS1-2; PS-2; familial Alzheimer's disease; cerebral haen depression; antibody; gene expression modul Homo sapiens. W09534099-A2. 31-0C1-1996; CA0263. 28-JPR-1995; US-496841. 31-JUL-1995; US-296841. 31-JUL-1995; US-296841. 31-JUL-1995; US-296841. 31-JUL-1995; US-296841. 31-JUL-1995; US-296841. 31-JUL-1995; US-496841. 31-JUL-1995; US-296841. 31-JUL-1996; US-296841. 31-JUL-1996; US-296841. 31-JUL-1996; US-296841. 31-JUL-1996; US-296841. 31-JUL-1996; US-296841. 31-JUL-1996; US-296841. 31
O H C M 와 U	80

DRYVCSGVPGRPPGLEEELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLI

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New isolated mutant presentiin-1 genes - useful for developing products for use in detection, diagnosis and therapy of Alzheimer's disease and for drug screening

"I disease and for drug screening
"I disease and for drug screening
"I claim 19; Page 203-204; 238pp; English.
"This polypeptide comprises human presentlin-2 (hPS2). Its amino and sequence was deduced from an isolated cDNA clone (see V04669). Human and mutine presentlin-1 sequences are also provided (see W23964-66). Mutations in the PS-1 and PS-2 genes are linked to the development in humans of forms of familial Alzheimer's disease (FAD) and may be causative of other disorders, e.g. cognitive, intellectual, neurological or physiological disorders such as crebral haemorrhage, schizophrenia, depression, mental retardation and epilepsy. Use of the nucleic acids and proteins comprising or derived from the presentlins is made in screening and diagnosing FAD, identifying and developing therapeutics for treatment of FAD, complishing cell lines and transgenic animals useful as models of FAD. Methods for identifying substances that bind to, or modulate the activity of a presentlin protein, and methods for presently in witherapetin with a presently protein with protein with protein with a presently in the presently or a presently in the presently or a pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            presentiin interacting protein with a presentlin protein are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "Asn14111e mutation site (Claim 19)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "Met239Val mutation site (Claim 19)"
                                                                                                                                                                           225. .244
/label= TM5
/note= "transmembrane domain 5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note- "transmembrane domain 8"
                                                                                      /note= "transmembrane domain 4"
                                                                                                                                                                                                                                                                                                                                                           /note= "transmembrane domain 6"
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12-JUL-1996; US-0217700.
08-NOV-1996; US-029895.
(HSCR-) HSC RES & DEV LP.
(UTOR) UNIV TORONTO GOVERNING COUNCIL.
FIRSET PE, RORMENES JM, St GEOTGE-HYSIOP PH;
WPI; 98-286355/25.
                                                                                                                                                                                                                                                                                                                                                                           269. .387
/label- TM6-7
/note- "hydrophilic loop"
/label= TM3-4
/note= "hydrophilic loop"
                                                                                                      719. .224
/label= TM4-5
/note= "hydrophilic loop"
                                                                                                                                                                                                                                             245. .249
/label= TM5-6
/note= "hydrophilic loop"
                                                                                                                                                                                                                                                                                                             250. .268
/label= TM6
                                                                    /label- TM4
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/label= TM
                                             .218
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04-JUL-1997; 0
02-JAN-1997; 1
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Sequence
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ö 0; Gaps 100.0%; Score 2336; DB 1; Length 448; 100.0%; Pred. No. 7.3e-237; ive 0; Mismatches 0; Indels 0 Query Match 100. Best Local Similarity 100. Matches 448; Conservative

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1 MLTFMASDSEEEVCDERTSLMSAESPTPRSCQEGRQGPEDGENTAQWRSQENEEDGEEDP

New presention genes - useful for diagnosis, therapy and drug
PT screening of familial Alzheimer's disease, cerebral disorders, etc.
Claim 4: 178pp. English.
CC Mighly conserved integral membrane proteins with a common structural
CC fighly conserved integral membrane proteins with a common structural
CC fighly conserved integral membrane proteins with a common structural
CC fighly conserved integral membrane proteins with a common structural
CC fighly conserved integral membrane proteins with a common structural
CC disease (AD) and possibly other diseases such as cerebral haemorrhage,
CC disease (AD) and possibly other diseases such as cerebral haemorrhage,
CC diseases. The wild type sequences can be used for diagnosis of these
CC diseases. The wild type proteins, or vectors that express them or
CC containing antisense sequences, antibodies selective for these mutant
CC forms of the proteins and modulators of PS gene expression are
CC optentially useful for treatment of AD etc. Transgenic animals are useful
CC affinity purification and in immunoassays.
SQ Sequence 448 AA; Presentlin-2 M239V mutation.
Presentlin-2; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; AD; familial Alzheimer's disease; cerebral haemorrhage; schizophrenia; depression; antibody; gene expression modulator; therapy; mutein. YTPFTEDTPSVGQRLLNSVLNTLIMISVLVVMTJFLVVLYKYRCYKFIHGWLIMSSLMLL FLFTYIYLGEVLKTYNVAMDYPTLLLTVWNFGAVGMVCIHWKGPLVLQQAYLIMISALMA FLFTYIYLGEVLKTYNVAMDYPTLLLTVWNFGAVGMVCIHWKGPLVLQQAYLIMISALMA LVFIKYLPEWSAWVILGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVW TVGMAKLDPSSQGALQLPYDPEMEEDSYDSFGEPSYPEVFEPPLTGYPGEELEEEEERGV KLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLTLLLLAVFKKALPALPISI 28-ARR-1995; US-431048. 28-JUN-1995; US-496641. 31-JUL-1995; US-509399. (HSCR-) HSC RES & DEV LP. (UTOR) UNIV TORONTO GOVERNING COUNCIL. TFGLIFYFSTDNLVRPFMDTLASHQLYI 448 Location/Qualifiers W05763 standard; Protein; 448 AA. /label- M239V 29-APR-1996; CA0263 modified_site Homo sapiens. WO9634099-A2. 25-JUL-1997 W05763; 421 61 181 181 241 301 301 361 361 121 RESULT 셤 ð 용 ò ò 용 à 셤 ò à 셤 셤

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                                                                                                                                useful
regions. Mutations in PS genes are implicated in familial Alzheimer's disease (AD) and possibly other diseases such as cerebral haemorrhage, schizophrenia, depression etc., so detection of mutations in the DNA encoding the wild type sequences can be used for diagnosis of these diseases. The wild type proteins, or vectors that express them or containing antisense sequences, antibodies selective for these mutant forms of the proteins and modulators of PS gene expression are potentially useful for treatment of AD etc. Transgenic animals are usef as models for drug screening. The antibodies can also be used e.g. for Sequence 448 AA;
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Identifying genes which cause improper chromosome segregation,
screening for inhibitors of chromosome missegregation and processes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TVGMAKLDPSSQGALQLPYDPEMEEDSYDSFGEPSYPEVFEPPLTGYPGEELEEEEERGV
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                                                                                                                                                                                                                           Length 448;
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Pred. No. 6.4e-236;
0; Mismatches 1;
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AD3; AD4/AD3LP; Alzheimer's disease; chrom presenilin; inhibitor; AD; trisomy 21; ss.
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Local Similarity 99.8%;
Nes 447; Conservative
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07-DEC-1997 (first entry)
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15-AUG-1996, U13314.
16-AUG-1995, US-002448.
(HARD ) HARVARD COLLEGE.
Li J, Potter H:
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N-PSDB; T87426.
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WO9707213-A2.
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25-JUL-1997 (first entry)
Presentlin-2 delta263-296 mutation.
Presentlin-2; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; AD;
familial Alzhelmer's disease; cerebral haemorrhage; schizophrenia;
depression; antibody; gene expression modulator; therapy; mutein.
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                                                                                                                                                                                                                                                                                                                    YTPFTEDTPSVGQRLLNSVLNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 TVGMAKLDPSSQGALQLPYDPEM-EDSYDSFGEPSYPEVFEPPLTGYPGEELEEEERGV 359
                                                                                                                                                                        Gaps
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W05763-W05766 represent mutated versions of the human presentlin-2
                                                                28
                                                                                                                                                                                                   1 MLTFMASDSEEEVCDERTSLMSAESPTPRSCQEGRQGPEDGENTAQWRSQENEEDGEEDP
                                                                                                                                                                                                                    1 MLTFWASDSEEEVCDERISIMSAESPIPRSCQEGRQGPEDGENTAQWRSQENEEDGEEDP
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                                                                                                                                         DB 1; Length 447;
was exemplified using Alzheimer's disease. The sequences given in T87401 to T87426 can be used in the above methods. It is not clear from the figure legend, the figure and the disclosure of the specification which sequence of Fig 1 and is the AD4/AD31P or the AD3 sequence.
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/note= "site of 34 residue deletion"
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                                                                                                                                         99.3%; Score 2320.5; DB 1
99.8%; Pred. No. 3.1e-235;
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(HSCR-) HSC RES & DEV LP.
(UTOR ) UNIV TORONTO GOVERNING COUNCIL.
Fraser PE. Rommens JM, St George-Hyslop PH;
                                                                                                                                                                      0; Mismatches
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US-496841.
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29-APR-1996; CA0263.
                                                                                              447 AA;
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28-JUN-1995;
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24 ESPIPRSCQEGRQGPEDGENTAQWRSQENEEDGEEDPDRYVCSGVP----GRPPG---- 75
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Matches 299; Conservative
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04-JUL-1997; C
02-JAN-1997; U
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coding sequence for wild type human PS-2. The presentlins are a family of highly conserved integral membrane proteins with a common structural nortif, common alternate splicing patterns, and common mutational hot spot regions. Mutations in PS genes are implicated in familial Albheimer's disease (AD) and possibly other diseases such as cerebral haemorrhage, schizophrenia, depression etc., so detection of mutations in the DNA encoding these sequences can be used for diagnosis of these diseases. These proteins, or vectors that express them or containing antisease sequences, antibodies selective for mutant forms of these proteins (such as W05736) and modulators of PS gene expression are potentially useful for treatment of AD etc. Transgenic animals are useful as models for drug screening. The antibodies can also be used e.g. for affinity purification
                                                                                                                                                                                                                                                                                                                                                                                            248
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                                                                                                                                                                                                                                                             | | | | : | | | :: | | | : : | | | EIPAPLSYFQNAQMSEDSHSSSAIRSQNDSQERQQQHDRQRLDNPEPISNGRPQSNSRQV
                                                                                                                                                                                                                                                                                              -----LEEELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFTEDT
                                                                                                                                                                                                                                                                                                         63 VEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVAIIKSVSFYTRKDGQLIYTPFTEDT
                                                                                                                                                                                                                                                                                                                                                                                          GEVLKTYNVAMDYPTLLLTVWNFGAVGMVCIHWKGPLVLQQAYLIMISALMALVFIKYLP
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Mouse presenilin-1 homologue.
Presenilin-1; PS1 gene; mouse; familial Alzheimer's disease;
cerebral haemorrhage; schizophrenia; depression; epilepsy;
mental retardation; diagnosis; therapy; transgenic animal.
                                                                                                                                                                                                  Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSSQGALQLPYDPEME-----EDSYDSFGEPSYPEVFEPPLTGYPG----
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                                                                                                                                                                                               62.8%; Score 1468; DB 1;
64.0%; Pred. No. 9.9e-146;
iive 46; Mismatches 78;
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/label= TM1
/note= "transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101. .132 /label= TM1-2 /note= "hydrophilic loop" | 133. .154
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                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 299; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus.
Key
                                                                                                                                                              Sequence
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disease and for drug screening, drughosts and therapy of nightering bisclosure; Page 199-200; 238pp; English.

This polypeptide comprises the murine presentlin-1 (PS1) homologue. Its amino acid sequence was deduced from an isolated cDNA clone (see V04668). Mutations in the human PS1 and PS2 genes (see V04666-68) have been linked to the development in humans of forms of familial Alzheimer's disease (FAD). All amino acids that are mutated in analysed FAD pedigrees (see W2364) were conserved in the murine homologue. Use of the nucleic acids and proteins comprising or derived from presentlins can be made in screening and diagnosing FAD, identifying and developing therapeutics for treatment of FAD, and in producing cell lines and transgenic animals useful as models of FAD. Methods for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated mutant presention-1 genes - useful for developing products for use in detection, diagnosis and therapy of Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              substances that bind to, or modulate the activity of a presentlin protein, and methods for identifying substances that affect the interaction of a presentlin-interacting protein with a presentlin protein are also disclosed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note- "Phel77Ser mutation site (Claim 1)"
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                                                                            /label= TM3
/note= "transmembrane domain 3"
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                                                                                                                                                                                                                                           /label= TM4
/note= "transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                         "transmembrane domain
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08-NOV-1996; US-029895.
(HSCR-) HSC RES & DEV LP.
(TOR.) UNIV TORONTO GOVERNING COUNCIL.
Fraser PE, Rommens JM, St George-Hyslop PH;
                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-
239, .243
/label= TM5-6
.** "hydrophilic loop"
                                                                                                                               184. .154
/label= TM3-4
'~~te= "hydrophilic loop"
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/note= "hydrophilic loop"
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/note= "hydrophilic loop"
                      'note= "hydrophilic loop
/label= TM2-3
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/label= TM8
                                                                                                                                                                                                                                                                                                                                                                                                                /label- IM5
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                                                   .183
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US-021673.
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N-PSDB; V04668.
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Gaps

44;

78; Indels

Length 467;

62.8%; Score 1468; DB 1; 64.0%; Pred. No. 9.9e-146;

46; Mismatches

/label= TM3

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peptides. Antisense nucleic acid may also be used to regulate expression of the PS1/429 gene, and both nucleic acids and peptides are useful as size markers in electrophoresis, chromatography etc. The transgenic animals are used as models for Ab. e.g. for testing drugs. Regulators of the PS1/429 gene or polypeptide can be used to treat e.g. Ab or diseases involving mitochondrial pathology, apoptosis and neurodegeneration. Typical regulators are antisense sequences, ribozymes, aptamers, synthetic or natural compounds. (II) may also be used to target other coding sequences to particular cellular locations.
                                                                                                                                                                                                                                                                                                                241
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QELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCLT 421
                                                                                                                                                                                                          -----LEEELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFTED 127
                                                                                                                                                                                                                      TPSVGQRLLNSVLNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIY 187
                                                                                                                                                                                                                                                              LGEVLKTYNVAMDYPTLLLTVWNFGAVGMVCIHWKGPLVLQQAYLIMISALMALVFIKYL 247
                                                                                                                                                                                                                                                                                                                                   PEWSAWVILGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWTVGMAKL 307
                                                                                                                                                                                                                                                                                                                                                      PEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAEG 301
                                                                                                                                                 Gaps
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                                                                                                                                                                   24 ESPTPRSCQEGRQGPEDGENTAQWRSQENEEDGEEDPDRYVCSGVP----GRPPG---- 75
                                                                                                                                                                                                                                                                                                      DPSSQGAL--QLPYDPE-MEEDSYDSFGE---PSYPEVFEPPLTGYPG------
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Human presenilin-1.
Presenilin-1; PSI gene; human; familial Alzheimer's disease; FAD;
                                                                                                                                                42;
                                                                                                                         Query Match 62.8%; Score 1467; DB 1; Length 467; Best Local Similarity 65.7%; Pred. No. 1.3e-145; Matches 306; Conservative 39; Mismatches 79; Indels 4
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mental retardation; dlagnosis; therapy; transgenic animal
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/label= TM1
/note= "transmembrane domain
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155. .163
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/note= "hydrophilic loop"
164. .183
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/label= TM1-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "residue 258-290 deletion mutant, as
with Asp257Ala mutation (Claim 1)"
                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "lle439Val mutation site (Claim 1)" Misc_difference 257
                                                                                                                                                                                                                                                                                                                                                                                                    'note= "Phell7Ser mutation site (Claim 1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               residue 258-290 deletion (Claim 1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Asp257Ala mutation site,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Met146Leu mutation site
Misc_difference 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Pro264Leu mutation site
Misc_difference 267
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                                                                           /label= TM4
/note= "transmembrane domain
                                                                                                                                                                    /label- TM5
/note- "transmembrane domain
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/note= "transmembrane domain
'note= "transmembrane domain
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              184. .194
/label= TM3-4
/note= "hydrophilic loop"
                                                                                                                                                                                                                  /label= TM5-6
/note= "hydrophilic loop'
                                                                                                                                                                                                                                                                                         263. .407
/label- TM6-7
/note= "hydrophilic loop"
                                                                                                                                      'note= "hydrophilic loop
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/label= TM
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Misc_difference 139
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Gaps	75	RQ 61	ED 127	ED 121	IY 187	IY 181	XL 247	 YL 241	KL 307	EG 301	350	AV 361	LT 402	 LT 421		
42;	RPPG	II I RPQGNS	IYTPFT	IYTPFT	LFLFTY	LFFFSF	ALVFIK	ALVFIK	WIVGMA	STMVWLVNMAE		TPESRA	ILIGEC	ILIGEC		
Indels	DďA	HPEPLSNG	YTEKNGOL	YTRKDGQL	LIMSSLML	TIISSIT	LIMISALM	LIMISALM	LIYSSAMV	VIYSSTMV	GYPG	SHLGPHRS	TTLACEVA	TITACEVA	XI 448	YI 467
79;	RYVCSG	RR-SLG	IKSVRE	IKSVSF	KFIHGW	KVIHAW	VLQQAY	RLQQAY	EPIFPA	ETLEPA	FEPPLT	: I WEAQRD	GSGDWN	ASGDWN	LASHOL	
40; Mismatches	ESPTPRSCOEGROGPEDGENTAQMRSOENEEDGEEDPDRYVCSGVPGRPPG	ELPAPLSYFONAQMSEDNHLSNTVRSQNDNRERQEHNDRR-SLGHPEPLSNGRPQGNSRQ		62 VVEQDEEEDEELILKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTED	TPSVGQRLLNSVLNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLINSSLMLLFLFTYIY	TETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLFFFSFIY	LGEVLKTYNVAMDY PTLLLTVWNFGAVGMVCIHWKGPLVLQQAYLIMISALMALVPIKYL	LGEVFRTYNVAVDYITVALLIWNFGVVGMISIHWRGPLRLQQAYLIMISALMALVFIKYL	PEWSAWVILGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWTVGMAKL	PEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLEPAVIXSSTMVWLVNMAEG	DPSSQGALQLPYDPE-MEEDSYDSFGEPSYPEVFEPPLTGYPG	DPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAV	EELEEBEBERGVKLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILLGLCLT	: QELSSSILAGEDPEERGVKLGLGDF1FYSVLVGKASATASGDWNTTIACFVAILIGLCLT	LLLLAVFKKALPALPISITFGLIFYFSTDNLVRPFWDTLASHQLYI	LLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI
40;	PAOWRS	SNTVRS	IMLEV	/IMLEV	TWVNI'	IVVMT	WNFGA	WNFGV	CPKGP	CPKGP	DSYDS	ERESODTV	LGDFI	LEDEI	SLIFYE	LVFYE
Conservative	ROGPEDGENT	AQMSEDNHLS	CTLKYGAKHV	LTLKYGAKHV	VLNTLIMIS	LINAAIMISV	WOYPILLITY	DYITVALL	ISVYDLVAVI	ISVYDLVAVI	LPYDPE-MEE	SKYNAESTER	SEEERGVKLO	PEERGVKLO	PALPISITE	PALPISITE
Conse	SCOEG	SYFON	-LEEE	EEDEE	RLLNS	RALHS	TYNVA	TYNVA	VILGA:	LILAV	ALQ	RVSKN	E -	ILAGE	FKKAL	FKKAL
305;	ESPTPR	ELPAPL		VVEQDE	TPSVGQ	TETVGO	LGEVLK	LGEVFK	PEWSAW	PEWTAW	DPSSQG	DPEAQR	EEL	QELSSS	LLLLAV	LLLLAI
Matches	24	m	75	62	128	122	188	182	248	242	308	302	350	362	403	422
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Search completed: March 20, 2000, 05:31:20 Job time: 4209 sec

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STRANDEDNESS:
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Query Match
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Sequence 137, App
Sequence 29, Appl
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Sequence 138, App
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                                                                                   US-08-509-359B-137
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1 MLTFMASDSEEEVCDERTSL.....STDNLVRPFMDTLASHQLYI 448
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/cgn2_6/ptodatua/2/laa/5B_COMB.pep:*
/cgn2_6/ptodatua/2/laa/pcTUG9_COMB.pep:*
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       GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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    protein search, using sw model

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Sequence 2, Sequence 2, Sequence 2, Sequence 4, Sequence 6, Sequence 6, Sequence 6,
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Patent No. 5840540
GENERAL INFORMATION:
APPLICANT: ROWGENS, JOHANNA M
APPLICANT: RASER, PAUL E
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREE: High Street Tower - 125 High Street
CONTY: Boston
STATE: Massachusetts
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-NOV-1997
CLASSIFICATION 435
PRIOR APPLICATION NUMBER: 08/592,541
FILING DATE: APPLICATION NUMBER: 08/592,541
US-08-136-742A-2
US-08-135-80AA-2
US-08-951-912-2
US-08-951-912-4
US-08-951-912-6
US-08-691-605-2
US-08-691-605-2
US-08-691-605-2
S-240846-5
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Matches 448; Conservative
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                                               Length 447;
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APPLICANT: ST. COMMENS, JOHANNA M
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: RASER, PAUL E
TITLE OF INVENTION: GENERAL SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSE: TESTA, HURWITZ & THIBEBAULT
STREET: HIGH Street Tower - 125 High Street
                                            Score 2320.5; DB 2; Length
Pred. No. 4e-230;
0; Mismatches 0; Indels
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APPLICATION NUMBER: US/08/967,101
CLASSIFICATION: 435
**RIOR BATE: 10-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 TFGLIFYFSTDNLVRPFMDTLASHQLYI 448
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Pitcher, Edmund R. TELECOMMUNICATION INFORMATION:
                                             99.38;
99.88;
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                                       Ouery Match
Best Local Similarity 99.8
Matches 447; Conservative
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STATE: Massa
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US-08-875-972-29
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                                                                                                                                                                                                                                                                Length 372;
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Patent No. 5986634
CENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                          Indels
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PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                              82.3%; Score 1923; DB 2;
100.0%; Pred. No. 2e-189;
iive 0; Mismatches 0;
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STREET: High Street Tower - 125 High Street
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APPLICATION NUMBER: US/08/592,541
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ZIP: 0.2110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS OF SOFTWARE: Patrally
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 138:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                         LENGIH: 372 amino acids
                                                                                                                                                                                                                                                                Query Match 82.3
Best Local Similarity 100.
Matches 372; Conservative
                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-967-101-138
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STATE: Massachusetts
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High Street Tower
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STRANDEDNESS: si
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                                                   U.S.A.
                    Boston
                                                                 ZIP: 02110
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US-08-670-964-2
                                                  COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302 DPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAV 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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US-08-592-541-134

| Sequence 134, Application US/08592541
| Sequence 134, Application US/08592541
| Patent No. 5966054
| GENERAL INFORMATION:
| APPLICANT: ST. GEORGE-HYSLOP, PETER H
| APPLICANT: RRASEN, PAUL E
| TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
| TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
| NUMBER OF SEQUENCES: 183
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: TESTA, HURMITZ & THIBEAULT
                                                                                                                                                                                                                                                                                                                                                                                                                           42;
                                                                                                                                                                                                                                                                                                                                                                                     62.8%; Score 1467; DB 2; Length 467; 65.7%; Pred. No. 2e-142; Live 39; Mismatches 79; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              403 LLLLAVFKKALPALPISITFGLIFYFSTDNLVRPFMDTLASHQLYI 448
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                                                                                                                                                                                                                                                                                                                                                                                          /;
2e-142;
79;
PatentIn Release #1.0, Version #1.30
            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 anino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 306; Conservi
                                                                                                                                                                                                                                                                                   STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                       US-08-967-101-134
SOFTWARE:
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182 IGEVERTYNVAVDYITVALLIWNFGVVGMISIHWRGPLRLQQAYLIMISALMALVFIKYL 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 -----LEEELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFTED 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 DPEAORRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAORDSHLGPHRSTPESRAAV
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Patent No. 6010874
CENERAL INFORMATION
TITLE OF INVENTION: EARLY ONSET ALZHEIMER'S DISEASE
                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 62.8%; Score 1467; DB 2; Best Local Similarity 65.7%; Pred. No. 2e-142; Matches 306; Conservative 39; Mismatches 79;
- 125 High Street
                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              467 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                  Massachusetts
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CLASSIFICATION: 800
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Gaps

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242 PEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAEG 301
                                                                                                                                                          || :|  : | : | | | | | | 302 DPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAV 361
                                                                                                                                                                                                                               362 QELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCLT 421
                                                                                                                                     DPSSQGAL--QLPYDPE-MEEDSYDSFGE---PSYPEVFEPPLTGYPG------
                                                                                                                                                                                                               EEL-----EEEEERGVKLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLT
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                                                                                                                                                                                                                                                                                        LLLLAVFKKALPALPISITFGLIFYFSTDNLVRPFMDTLASHQLYI 448
                                                                                                                                                                                                                                                                                                         APPLICANT: Hardy, John A.
TITLE OF INVENTION: EARLY ONSET ALZHEIMER'S DISEASE
ITLILE OF INVENTION: GENE AND GENE PRODUCTS
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road - UW2220; P.O. Box 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.2%; Score 1454; DB 3;
65.3%; Pred. No. 4.2e-141;
iive 40; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-670-964-4; Sequence 4, Application US/08670964; Patent No. 6010814; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34,344
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TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Han, William T
REGISTRATION NUMBER: 34,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
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Matches 303; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 610-270-5090
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MOLECULE TYPE: protein
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 ELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRR-SLGHPEPLSNGRPQGNSRQ 61
                                             302 DPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAAV
                                                                                                               350 EEL-----EEEEERGVKLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLT
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                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ROWNES, JOHANNA M
APPLICANT: ROWNES, JOHANNA M
APPLICANT: FRASER, PAUL
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80; Indels
                                                                                                                                                                    403 LLLLAVFKKALPALPISITFGLIFYFSTDNLVRPFMDTLASHQLYI 448
                                                                                                                                                                                          422 LLLLAIFKKALPALPISIIFGLVFYFATDYLVQPFWDQLAFHQFYI 467
                   DPSSQGAL -- QLPYDPE-MEEDSYDSFGE---PSYPEVFEPPLTGYPG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.5%; Score 1461; DB 2;
65.5%; Pred. No. 8.1e-142;
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gh Street Tower - 125 High Street
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                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08592541
Patent No. 5986054
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High Street Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (6/7) 248-7100
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 65.58
Matches 305; Conservative
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TOPOLOGY: linear
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CLASSIFICATION: 800
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02110
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Search completed: March 18, 2000, 19:55:31
Job time: 3229 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVLKTYNVAMDYPTLLLTVWNFGAVGMVCIHWKGPLVLQQAYLIMISALMALVFIKYLPE 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L-----EEEEERGVKLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLTLL 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 ELPAPLSYFONAOMSEDNHLS---NTNDNRERQEHNDRRSLGHPEPLSNGRPQGNSRQVV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 ESPTPRSCQEGRQGPEDGENTAQWRSQENEEDGEEDPDRYVCSGVP---GRPPG----75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42;
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Sequence 4, Application US/08967101
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Sequence 4, Application Content Conten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.5%; Score 1437; DB 2; Length 46
64.9%; Pred. No. 2.3e-139;
Live 41; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              405 LLAVFKKALPALPISITFGLIFYFSTDNLVRPFMDTLASHQLYI 448
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STREET: High Street Tower - 125 High Street
P50361
                        TELECOMMUNICATION INFORMATION TELEPHONE: 610-270-5219 TELEFAX: 610-270-5090
REFERENCE/DOCKET NUMBER:
                                                                                                                                         INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                               FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-670-479-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 301; Conservative
                                                                                                                                                                                                                                                                            TOPOLOGY: Ilneur
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                          STRANDEDNESS: single
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Best Local 9
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| :| ::| :| :| 303 PEAQ--RRVPKNPKNPKNTQRAERETQDSGSGNDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 PSVGQRLLNSVLNTLIMISVIVVMTIFLVVLYKKYRCYKFIHGWLIMSSLMLLFLFTYIYL 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 ESPTPRSCQEGRQGPEDGENTAQWRSQENEEDGEEDPDRYVCSGVP----GRPPG---- 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GEVLKTYNVAMDYPTLLLTVWNFGAVGMYCIHWKGPLVLQQAYLIMISALMALVFIKYLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               350 -EEL-----EEEEERGVKLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 -----LEEELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFTEDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSSQGALQLPYDPEME-----EDSYDSFGEPSYPEVFEPPLTGYPG-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PATENTIN Release #1.0, Version #1.30
APPLICATION NOMBER: US/08/967,101
FILING DATE: 10-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 1418; DB 2;
; Pred. No. 2.1e-137;
48; Mismatches 86;
                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                     TELEPHONE: (617) 246-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.7%;
61.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 61.94
Matches 289; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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- protein search, using sw model OM protein March 18, 2000, 14:03:43 ; Search time 41.25 Seconds
 (without alignments)
512.287 Million cell updates/sec on: Run

US-08-509-359B-137 2336 1 MLTFMASDSEEEVCDERTSL.....STDNLVRPFMDTLASHQLYI Perfect score: Sequence:

448

BLOSUM62 Scoring table: 142080 segs, 47169319 residues Searched:

PIR_62:*

Database :

0 Word size :

142080 •• Number of hits that pass the threshold
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description		7	seven trans-membra	presenilin-beta -	끆	in 1	Н	in-	<u>"</u>	n.	spl,	무	hypothetical prote	presentlin homolog	sperm membrane pro	hypothetical prote	Œυ	um channel	ransport	c fibrosis	£1]	potassium transpor	Ω	ubiquinolcytochr	bride of sevenless	ubiquinolcytochr	sodium channel mNa	sodium channel pro	_	isp4 protein homol	integrin-associate	cytochrome-c oxida	serotonin receptor	sodium channel pro	probable amino aci
SUMMAKIES		ΠD	158098	A56993	139174	JC5391	178388	S58396	563683	JC5390	JC5080	JC5081	S63684	S60253	T15184	T00724	A43459	T11596	A38195	CHRTM1	H75043	A39901	A40303	T02268	JC6139	S47882	A47550	I48135	A55138	800320	A60054	T01900	S36646	E70488	JC6178	A33996	T11710
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		Length	448	448	442	449	467	467	463	433	467	463	374	461	358	453	465	531	2016	1840	398	1476	1476	826	1450	382	893	379	1681	1951	1983	166	324	592	379	2019	521
æ	Query		100.0							62.1												٠	•	٠	4.4	•		•	4.3		4.3	٠	4.3	•	4.3	٠	•
		Score	2336	23	2215.5	624	4	4	14	1449.5	マ	7	സ	O,	524.5	513	274	119	110	109	106	104	104	٦,	103.5	7	102.5	٦,	5	100.5	8	8	8	100	99.5	66	თ თ
	Result	0	Н	7	m	4	υ.	ø	7	α		10			13	14	15	16	17	18	19	20	21	22	23	24	25	5 6	27	28	58	30	31	32	93	34	32

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TVGMAKLDPSSQGALQLPYDPEMEEDSYDSFGEPSYPEVFEPPLTGYPGEELEEEERGV

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KLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLTLLLLAVFKKALPALPISI

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111829 Sodium channel alp sodium channel alp sodium channel alp 151964 Sodium channel alp hypothetical prote voltage-gated sodi endothelin recepto ubiquinolcytochr S52968 NADH dehydrogenase	ALIGNMENTS	RESULT 1 158098 E5-1 protein - human C;5pecies: Homo saplens (man) C;5pecies: Homo saplens (man) C;becies: Homo saplens C;Accession: 158098 C;Accession: 1448 C;Accession: 158098 C;Access	Score 2336; DB 2; Length 448; Pred. No. 8.1e-167; 0; Mismatches 0; Indels 0; Gaps 0;	MLTEMASDSEEEVCDERTSLMSAESPTPRSCQEGROGFEDGENTAQWRSQENEEDGEEDP 60
0000000000) R.; i Frase; s dise MUID:: lated		SLMSA SLMSA
461 1836 1836 1836 1835 1695 1695 441		#sequence_revision trington, R.; Rogaev 11, L.; Fraser, P.E 1995 Zhelmer's disease 158098; MUID:953795 y; translated from ES> GB:L44577; NID:9956	vat	CDERT
4444444444		1098 1 protein - human 2 pecies: Homo sapiens (mar 3 pecies: Homo sapiens (mar 3 pecies: 10.7 Jul-1996 #sequenc 6 pecies: 158098 6 pecies: 158098 775-778, 1995 775-778, 1	7	ASDSEEEN ASDSEEEN
99999999999999999999999999999999999999		SULT 1 8098 -1 protein - Species: Homo Species: Homo Accession: I5 Rogaev, E.I.; Cohen, D.; L. Ture: Famili Reference num Reference num Reference num Reference num Residues: 1-4 Cross referen Genetics: Genetics: Superfamily:	Match Jocal Sin	1 MLTEM 1 HIII 1 MLTEM
3 3 3 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		RESULT 1 158098 E5-1 protein - human C;Species: Homo sapiens (man) C;Date: 02-Jul-1996 #sequence_rev C;Accession: 158098 R;Rogaev, E.I.; Sherrington, R.; Cohen, D.; Lannfelt, L.; Frase Nature 376, 775-778, 1995 A;Title: Familial Alzheimer's dis A;Reference number: 158098; MUID: A;Accession: 158098 A;Status: preliminary; translated A;Residues: 1-448 (RES> A;Cross-references: GB:L44577; NI C;Superfamily: presenilin	Query Match Best Local Matches 44	Qy Db
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249 EWSAWVILGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWTVGMAKLD [1: 1: 1: 1	Db 361 VQELSGSILTSEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420 QY 402 TLLLLAVFKKALPALPISITFGLIFYFSTDNLVRPFMDTLASHQLYI 448	RESULT 6 528396 presentlin 1, splice form 467 - human N.Alternate names: Alzheimer's disease protein 3; protein S182 C;Species: Homo sapiens (man) C;Species: J9-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 29-Sep-1999 C;Accession: S58396; S71401; S71402 R;Sherrington, R.; Rogaev, E.I.; Lidang, Y.; Rogaeva, E.A.; Levesque, G.; Ikeda, M.; C ero, I.; Pinessi, L.; Chumakov, I.; Pollen, D.; Brookes, A.; Sanseau, P.; Po	Nature 375, 754-760, 1995 AyTitle: Cloning of a gene bearing missense mutations in early-onset familial Alzheim A; Reference number: 158095; MUID:95319502 A; Accession: 558396 A; Moleype: MRNA A; Residues: 1.467 < SHE>	A; Cross references: EMBL:L42110; NID:9904118; PIDN:AAB46416.1; PID:9904119 R; Vidal, R.; Ghiso, J.; Wishiewski, T.; Frangione, B. FEBS Lett. 393, 19-23, 1996 A; Title: Alzheimer's presentlin 1 gene expression in platelets and megakaryocytes. Id A; Reference number: S71401; MID:95397521 A; Reference number: Reference number: S71401; MID:9401; M	24 ESFLENCESCAGE ELGENTAMEN SQUEDE ELGENTAGES PER CAFFORM STATE ST
7 SDSEEBVCDERTSLAMSAESPTPRSCOEGROGPEDGENTAQWRSOENEEDGEEDPDRYVCS [: : : : :	Db 117 EKDGQLIYTPFSEDTTSVGERLLNSVLNTLIMISVILVMTIFLVLLYKYRCYKFIHGWL1 176 QY 174 MSSLMLLFLFTYIXLGEVLKTYNVANDYPTLLLTVMNFGAVGMVCIHWKGPLVLQQAYL1 233	Oy 234 MISALWALVFIKYLEEWSAWVILGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALI 293 237 MISALWALVFIKYLEEWSAWVILGAISVYDLLAVLCPKGPLRMLVETAQERNEPIFPALI 296 Qy 294 YSSAWVWTVGMAKLDPSSQGALQLPYDPEMBEDSYDSFGEPSYPEVFEPPLTGY 347	Qy 408 VFKKALPALPISITEGLIFYESTDNLVRPFWDTLASHQLX1 448 	TRESULT 5 178388 180 protein - mouse 1. Species: Mas musculus (house mouse) 2. Species: Mas musculus (house mouse) 3. Accession: 178388 8. Sherrington, R.; Rogaev, E.; Lidang, Y.; Rogaeva, E.A.; Levesque, G.; Ikeda, M.; Chi, ero, I.: Pinessi, L.; Nee, L.; Chumakov, I.; Pollen, D.; Brookes, A.; Sanseau, P.; Pollen, E.; Rommens, J.M.; St George-Hyslop, P. H. 8.; Reference number: 158095; MUID:95319502 8.; Title: Cloning of a gene bearing missense mutations in early-onset familial Alzheimer' 8.; Reference number: 158095; MUID:95319502 8.; Accession: 178388 8.; Accession: 178388 8.; Accession: 178388 8.; Residues: 1-66. Access 8.; Active: prediminary; translated from GB/EMBL/DDBJ 8.; Residues: 1-67. Access 8.; Active: prediminary; translated from GB/EMBL/DDBJ 8.; Conservative 46; Mismatches 78; Indels 44; Gaps 6; 8.; Conservative 46; Mismatches 78; Indels 44; Gaps 6; 8.; Access access GB: 11 1 1 1 1 1 1 1 1 1	123 ETVGGRALHSILNAAIMISVIVIMTILLVVYKKRCKKVIHAWLIISSLLLEFFSFIXL 189 GEVLKTYNVAMDYPTLLITVNNFGAVGAVCIHWKGPIVLQQAVLIMISALMALVFIKKLP

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Across references: EMEL:271333
C;Comment: This protein is an intermembrane protein with seven transmembrane domains.
C;Comment: This protein is an intermembrane protein with seven transmembrane and office 
                                                         the presenilin 1 gene
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C'Species: Homo sapiens (man)
C'Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 29-Sep-1999
C'Accession: S63684
R'Sahara, N.; Yahagi, Y.; Takagi, H.; Kondo, T.; Okochi, M.; Usami, M.; Shirasawa, FEBS Lett. 381, 7-11, 1996
A'; Title: Identification and characterization of presenilin I-467, I-463 and I-374.
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357 VQEISSSIPASEDPEERGVKLGLGDFVFYSVLVGKASATASGDWNTTIACFVALLIGLCL
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        Biochem. Biophys. Res. Commun. 228, 430-439, 1996
A;Title: Molecular cloning, sequencing, and brain expression of
A;Reference number: JC5080; MUID:97079199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLLLLAVFKKALPALPISITFGLIFYFSTDNLVRPFMDTLASHQLYI 448
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64.2%; Pred. No. 4.7e-100;
tive 39; Mismatches 80;
                                                                                                                                                                                                                    not shown
                                                                                                                                  A, Contents: brain
A, Accession: JC5081
A, Status: nucleic acid sequence
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A; Residues: 1-463 <CAL>
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A; Accession: S63684
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Matches 300;
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A.Experimental source: brain
C.Comment: This protein is an intergral membrane protein with seven transmembrane domain
C.Goment: This protein is an intergral membrane protein with seven transmembrane domain
C.Goment: This protein is an intergral membrane protein with seven transmembrane domain
C.Goment: Silverfamily: presentiin
C.Superfamily: p
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                                                                                                                                                                               Bellis
presentin 1 protein isoform 467 - lesser mouse lemur

C.Species: Microcebus murinus (lesser mouse lemur)

C.Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 29-Sep-1999

C.Accession: JC5080

R.Calenda, A.; Mestre-Frances, N.; Czech, C.; Pradier, L.; Petter, A.; Bons, N.; Bochem. Biophys. Res. Commun. 228, 430-439, 1996

A:Title: Molecular cloning, sequencing, and brain expression of the presentlin 1 A:Accession: JC5080

A:Accession: 
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JC5081
presentlin 1 protein isoform 463 - lesser mouse lemur
C;Species: Microcebus murinus (lesser mouse lemur)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 13-Sep-1998
C;Accession: JC5081
R;Calenda, A.; Mestre-Frances, N.; Czech, C.; Pradier, L.; Petter, A.; Bons,
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64.4%; Pred. No. 1.4e-100;
iive 41; Mismatches 83;
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A,Title: Mutation of a putative sperm membrane protein in Caenorhabditis elegans prev A;Reference number: A43459; MUID:92407040
A;Reference number: A43459
A;Accession: A43459
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA; mRNA
A;Residues: 1-465 <LHE>
A;Cross-references: EMBL:214067; NID:96868; PID:96869; EMBL:214066; NID:96870; PID:96
A;Experimental source: strain Bristol N2
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
C;Genetics:
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                                                                                                                                                                                                                                                                                                                   Query Match 11.7%; Score 274; DB 2; Length 465; Best Local Similarity 21.5%; Pred. No. 3.4e-13; Matches 93; Conservative 80; Mismatches 127; Indels 132;
                                                                                                                                                                                                                                            A; Introns: 69/3; 154/3; 200/1; 224/3; 300/1; 386/1; 435/1
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                                                                                                                                      presentin homolog F22013.19 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 20-Sep-1999
C:Accession: T00724
R:Shinn, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; Concologis, A.; Ecker, J.R.
Submitted to the EMBL Data Library, April 1998
A:Reference number: 214200
A:Reference number: 214200
A:Reference number: zlazon
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-453 <SHI>
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C;Genetics:
A;Gene: ATSP:F22013.19
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A43459
Sperm membrane protein spe-4 - Caenorhabditis elegans
N.Alternate names: probable integral membrane protein
C;Species: Caenorhabditis elegans
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Sep-1997
C;Accession: A43459; S24632; S24633
B;L'Hernault, S.W.; Arduengo, P.M.
J. Cell Biol. 119, 55-68, 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 22.0%; Score 513; DB 2; Length 453; Best Local Similarity 31.1%; Pred. No. 5.2e-31; Matches 136; Conservative 78; Mismatches 130; Indels
    336 FYFSSHIALTPFTDLCTSQLILI 358
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C;Superfamily: presenilin
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OM protein - protein search, using sw model

March 18, 2000, 16:08:11; Search time 32.57 Seconds (without alignments) 410.791 Million cell updates/sec Run on:

US-08-509-359B-137
2336
1 MLTFMASDSEEEVCDERTSL....SIDNLVRPFMDTLASHQLYI 448 Title: Perfect score: Sequence:

Scoring table: BLOSUM62

82229 seqs, 29864866 residues Searched:

SwissProt_38:* Database :

0 Word size :

82229 Number of hits that pass the threshold : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	원	m snm		P79801 microcebus	xen	P49769 mus musculu				P79802 microcebus	_	Q20076 caenorhabdi	_	_	-	_				_	_		didelphis	_	Q24738 drosophila		_	pseudan						O20604 dasyurus ge	P15389 rattus norv		35673 phasc	43525 homo	
SUMMARIES		QI	PSN2_HUMAN	PSN2_MOUSE	PSN2_RAT	PSN2_MICMU	PSN2_XENLA	PSN1_MOUSE	PSN1_HUMAN	PSN1_RAT	PSN1_XENLA	PSN1_MICMU	FSN_DROME	YL4K_CAEEL	SEIZ_CAEEL	HOFI_CAEEL	PSNH_ARATH	SPE4_CAEEL	YDFG_SCHPO	CINS_HUMAN	CIN4_RAT	CYB_DASCR	CFTR_MOUSE	CFTR_RABIT	CYB_DIDMA	CYB_MICLO	BOSS_DROVI	CYBANTFL	CYB_DASMA	CYB_PSENI	CYB_NINYV	CYB_PARAP	CYB_PLAMS	CIN3_RAT	CYB_PSEMD	ட	LO.	CYB_ANTMI	CYB_PHATA	CIO3_HUMAN	CIN4_HUMAN
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ALIGNMENTS

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STRAIN-WISTAR; TISSUE-BRAIN;
MEDLINE; 97473536.
TAKAHASHI H., MERCKEN M., NAKAZATO Y., NOGUCHI K., MURAYAMA
IMAHORI K., TAKASHIMA A.;
"Cloning of cDNA and expression of the gene encoding rat
       STRAIN-WISTAR; TISSUE-BRAIN;
FRENTZEL S., ABDEL A.S., LUEBBERT H.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 95.3
Matches 427; Conservative
                                                                                                                       Gene 197:383-387(1997).
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                                                                                                                                                                                                                                                                                                                                 61 DRYVCSGVPGRPPGLEEELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLI 120
                                                                                                                                                                                                                                                                                                                                                              121 YTPFTEDTPSVGQRLLNSVLNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLL 180
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                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                        1 MLTFMASDSEEEVCDERTSLMSAESPTPRSCQEGRQGPEDGENTAQWRSQENEEDGEEDP
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                                                                                                                                                                                                                                     95.5%; Score 2232; DB 1; Length 448, 95.5%; Pred. No. 7.3e-147;
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                                                                                                                                                                                                                                                          14; Indels
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PSN2_RAT STANDARD; PRT; 448 AA.

O8977; 035546; 008947;

15-UL-1999 (Rel. 38, Created)

15-UL-1999 (Rel. 38, Last sequence update)

15-UL-1999 (Rel. 38, Last annotation update)

F PRESENILIN 2 (PS-2).

N PSEN2 OR PSNL2 OR PSN.2

S Rattus norvegicus (Rat).

C Eutharyota; Metazoa; Chordata; Craniata; Vertebrata; Mamm
                                                        PRESENILIN 2.
PRESENILIN 2-SHORT.
POTENTIAL.
                                                                                                                                                                         R -> H (IN REF. 2).
A -> V (IN REF. 2).
MISSING (IN REF. 2).
;; 680ACF19 CRC32;
                                                                                                                                                                                                                                                         6; Mismatches
                       MGD; MGI:100284; PSENZ.
PFAM; PF01080; Presentlin; 1.
Transmembrane; Alternative initiation.
CHAIN 1448 PRESENTLI
CHAIN 298 448 PRESENTLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TFGLIFYFSTDNLVRPFMDTLASHQLYI 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MW.
      EMBL; AF038935; AAB92660.1;
EMBL; U49111; AAC52935.1; -.
                                                                                                                                                                                                        49955
                                                                                                                                                                                                                                               Best Local Similarity 95.5
Matches 428; Conservative
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1D PSN2_RAT
1D PSN2_RAT
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                                                                                 TANAHASHI H., TABIRA T.;
"Cloning of the cDNA encoding rat presentlin-2.";
Blochim. Blophys. Acta 1396:259-262(1998).
-!- FUNCTION: MAY PLAY A ROLE
EXPRESSION OR IN LINKING CHROMATIN TO THE NUCLEAR MEMBRANE. MAY
FUNCTION IN THE CYTOPLASMIC PARTITIONING OF PROTEINS (BY
                                                                                                                                                                                                                                                                                     -i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
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R -> T (IN REF. 1).
KH -> ND (IN REF. 3).
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EMBL; D83700; BAA2283.1; -.
EMBL; AB004454; BAA20406.1; -.
PFAM; PF01080; Presenilin; 1.
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SEQUENCE FROM N.A.
STRAIN-WISTAR; TISSUE-BRAIN;
MEDLINE; 98207716.
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SHERRINGTON R., ROGAEV E.I., LIANG Y., ROGAEVA E.A., LEVESQUE G.,
SHERRINGTON R., ROGAEV E.I., LIANG Y., ROGAEVA E.A., LEVESQUE G.,
IKEDA M., CHI H., LIN C., LI G., HOLMAN K., TSUDA T., MAR L.,
FONCIN J.-F., BRUNI A.C., MONTESI M.P., SORBI S., RAINERO I.,
PINESSI L., NEE L., CHUMAKOV I., POLLEN D., BROOKES A.,
SANSEAU P., POLINSKY R.J., WASCO W., DA SILVA H.A.R., HAINES J.L.,
PERICKA-VANDE M.A., TAKZI R.E., ROSES A.D., FRASER P.E.,
ROMMENS J.M., ST GEORGE-HYSLOP P.H.;
"Cloning of a gene bearing missense mutations in early-onset familial
                                                                                                                                                                                                                                            293
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                                                                                                                          GVP-GRPPGL-------EEELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYT 113
                                                                    Gaps
                                                                                    7 SDSEEEVCDERTSLMSAESPIPRSCQEGRQGPEDGENTAQWRSQENEEDGEEDPDRYVCS 66
                                                                                                                                                                         - PPNGRISGADAYNSETTVENEEEELTLKYGARHVIMLFVPVTLCMVVVVAIIKSVSFYT
                                                                                                                                                                EKNGQLIYTPFTEDTPSVGQRLLNSVLNTLIMISVIVVMTIFLVVLYKYRCYRFIHGWLI
                                                                                                                                                                                                              348 PGEELEEEEERGVKLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLTLLLLA
                                                                                                                                                                                                    MSSLMLLFLFTY1YLGEVLKTYNVAMDYPTLLLTVWNFGAVGWVCIHWKGPLVLQQAYL1
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                                                                                              35;
                                               Length 449;
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                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                     409 VFKKALPALPISITFGLIFYFSTDNIVRPFMDTLASHQMYI 449
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                                                DB 1;
                                                                   .09
                                              69.5%; Score 1624.5; DB 1 ilarity 72.0%; Pred. No. 4.9e-105; Conservative 34; Mismatches 60;
POTENTIAL.
POTENTIAL.
DF6EAF4E CRC32;
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01-0cT-1996 (Rel. 34, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
PSENI OR PSNL1 OR AD3H.
                                                                                                                                                                                                                                                                                                                                                                                                                             467
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                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                   50274 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alzheimer's disease.";
Nature 375:754-760(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
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415
387
449 AA;
                                             Query Match
Best Local Similarity
Matches 332; Conserv
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P49769;
TRANSMEM
CARBOHYD
SEQUENCE
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PSN1_MOUSE
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44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 1468; DB 1;
; Pred. No. 3e-94;
46; Mismatches 78;
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MGD; MGI:1202717; PSEN1.
PFAM; PF01080; Presentiln; 1
Transmembrane; Glycoprotein.
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64.0%;
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Best Local Similarity 64.0%
Matches 299; Conservative
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LGEVLKTYNVAMDYPTLLLTVWNFGAVGMVCIHWKGPLVLQQAYLIMISALMALVFIKYL
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                                       "The Glu318Gly mutation of the presentlin-1 gene does not necessarily cause Alzheimer's disease.";
Ann. Neurol. 44:965-967(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POORKAJ P., SHARMA V., ANDERSON L., NEMENS E., ALONSO M.E., ORR H., WHITE J., HESTON L., BIRD T.D., SCHELLENBERG G.D., "Missense mutations in the chromosome 14 familial Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Missense mutation in exon 11 (codon 378) of the presentlin-1 gene in a French family with early-onset Alzheimer's disease and transmission study by mismatch enhanced allele specific amplification.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 99148656.
EZQUERRA M., CARNERO C., BLESA R., GELPI J.L., BALLESTA F., OLIVA R.;
"A presentlin 1 mutation (Ser169Pro) associated with early-onset AD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----LEEELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFTED 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANTS AD D-120; R-163; V-209; V-260; L-264; Y-410 AND P-426.
MEDLINE; 98180720.
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                                                                                                                                                                               ALDUDO J., BULLIDO M.J., FRANK A., VALDIVIESO F.;
"Missense mutation E318G of the presentlin-1 gene appears to nonpathogenic polymorphism.";
Ann. Neurol. 44:985-986(1998).
                                                                                                                                                                                                                                                                                                                                        CRUTS M., VAN DOIJN C.M., BACKHOVENS H., VAN DEN BROECK M., WEHNERT A., SERNEELS S., SHERRINGTON R., HUTTON M., HARDY J., ST GEORGE-HYSLOP P.H., HOFMAN A., VAN BROECKHOVEN C., Estimation of the genetic contribution of presentlin-1 and mutations in a population-based study of presentle Alzhenner
ROYTTA M., LILIUS L., EEROLA A., ST GEORGE-HYSLOP P.H., FREY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.8%; Score 1467; DB 1; Length 467; 65.7%; Pred. No. 3.5e-94; ive 39; Mismatches 79; Indels 4:
                                                                                                                                                                                                                                                                                           VARIANTS AD VAL-79; CYS-115; VAL-231, AND VARIANT GLY-318 MEDLINE; 98046005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 99211215.
BESANCON R., LORENZI A., CRUTS M., RADAWIEC S., STURIZ F.
BROUSSOLLE E., CHAZOT G., VAN BROECKHOVEN C., CHAMBA G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANTS AD LEU-169 AND GLN-436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hum. Mol. Genet. 7:43-51(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          presenilin 1 gene.";
Hum. Mutat. 11:216-221(1998).
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Neurology 52:566-570(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 65.7 es 306; Conservative
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                                                                                                                                                          MEDLINE; 99066775.
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                                                                                                                                     VARIANT GLY-318
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                                                                                                                        242 PEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNWAEG 301
                                                                                                                                                                                                                                                          362 QELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDMNTTIACFVAILIGLCLT 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 97199371.
TANIGUCHI T., HASHIMOTO T., TANIGUCHI R., SHIMADA K., KAWAMATA T., YASUDA M., NAKAI M., TERASHIMA A., KOIZUMI T., MAEDA K., TANAKA C.; Gene 186:73-75(1997).
248 PEWSAWVILGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWTVGMAKL
                                                                                                                                                                                                                   308 DPSSQGAL -- QLPYDPE-MEEDSYDSFGE---PSYPEVFEPPLTGYPG------
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-!- FUNCTION: MAY PLAY A ROLE IN INTRACELLULAR SIGNALING AND GENE EXPRESSION OR IN LINKING CHROMATIN TO THE NUCLEAR MEMBRANE.
MAY FUNCTION IN THE CYTOPLAGNIC PARTITIONING OF PROTEINS.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO THE PRESENTLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                              350 EEL-----EEEEERGVKLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLT
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TAKAHASHI H., MURAYAWA M., TAKASHIMA A., MERCKEN M., NAKAZATO Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammali:
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOGUCHI K., IMAHORI K.; "Molecular cloning and expression of the rat homologue of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          403 LLLLAVFKKALPALPISITFGLIFYFSTDNLVRPFMDTLASHQLYI 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-7UL-1999 (Rel. 38, Created)
15-7UL-1999 (Rel. 38, Last sequence update)
15-7UL-1999 (Rel. 38, Last sequence update)
15-7UL-1999 (Rel. 38, Last annotation update)
PRESENILIN I (PS-1) (S182 PROTEIN).
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EMBL, D82363; BAA11564.1; -.
PFAM, PF01080, Presenilin; 1.
Transmembrane; Glycoprotein.
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153
181
215
241
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                                                                                                                                                                                            62 VVERDEEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTED 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 TPSVGQRLLNSVLNTLIMISVIVVMTIFLVVLYKXRCYKFIHGWLIMSSLMLLFLFTYIY 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----LEEELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFTED 127
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                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Strepsirhini; Cheirogaleidae; Microcebus.
                                                                                                                                                                         CALENDA A., MESTRE-FRANCES N., CZECH C., PRADIER L., BONS N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1447; DB 1; Length 467;
Pred. No. 8.4e-93;
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A841A0B7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alternative splicing, Glycoprotein.
103 POTENTIAL.
153 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE PRESENILIN FAMILY
                              15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PSENI OR PSNLI OR PSI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Pred. No. 8.46
41; Mismatches
         467
                                                                                          Microcebus murinus (Lesser mouse lemur).
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64.4%;
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         STANDARD;
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467 AA;
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Best Local Similarity
                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                               MEDLINE; 97079199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane;
TRANSMEM 83
TRANSMEM 133
                                                                                                                                                   TISSUE-BRAIN;
         PSN1_MICMU
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                                                                                                                                                                                                                                                                                                                                                                                                                             402
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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"Characterization of Drosophila presentlin and its colocalization with Notch during development.";
submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
-! SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-! SIMILARITY: BELONGS TO THE PRESENILIN FAMILY.
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                                                                                                                                                                                          PEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAEG
                                                                                                                                                                                                                                                                                                                 || :| ; | | : : : | | : : : DPEAQRRVSKNTKYNAQGIEREAQASVPENDDGGFSEEWEAQRDSQLGPHRSISVSRAAV
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                                                                                                                                                                                                                                                                      DPSSQGAL--QLPYD-----PEMEEDSYDSFGEPSYPEVFEP----PLTGYPG
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BOULIANNE G.L., LIVNE-BAR I., HUMPHREYS J.M., LIANG Y., LIN ROGAEV E., ST GEORGE-HYSLOP P.; "Cloning and characterization of the Drosophila presentlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLLLAVFKKALPALPISITFGLIFYFSTDNLVRPFMDTLASHQLYI 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; 0/8004184; AAC33129.1; -.
EMBL; AF084184; AAC33129.1; -.
EMBL; AF084184; AAC33128.1; -.
FLYBASE; FBGN0019947; PS.
FTAM; PF01080; Presentlin; 1.
FTANSMEM 107 127 POTENTAL.
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15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          541 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (LONG ISOFORM).
MEDLINE; 97285868.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U77934; AAB61139.1; -.
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PSECULT 11
PSECULT 11
PSECULT 15-JUL
DT 15-JUL
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EEDSYDSF-----GE-----PSYPEVFEPP
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358 AA;
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                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
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Matches 117;
                                                                                                                                                                    HOP1_CAEEL
002100;
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TRANSMEM
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HOP1_CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                264 LVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWTVGMAKLDPSSQGALQLPYDPEM 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85 AKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQ-LIYTPFTEDTPSVGQRLLNSVLNTL 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144 IMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIYLGEVLKTYNVAMDYPT 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 PTPRSCQEGROGPEDGE-NTAQWRSQENEEDGEEDPDRYVCSGVPGRPPGLEEELTLKYG 84
                     Eukaryota, Metazoa; Nematoda; Secernentea; Rhabditía; Rhabditída; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                         LEVISIONS TO 84-85.
LEVITAN D.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY FACILITATE LIN-12 MEDIATED RECEPTION OF
INTERCELLULAR SIGNALS. IT MIGHT BE DIRECTLY INVOLVED IN LIN-12
MEDIATED RECEPTION, FUNCTIONING AS A CO-RECEPTOR OR AS A
DOWNSTREAM EFFECTOR THAT IS ACTIVATED UPON LIN-12 ACTIVATION.
ALTERNATIVELY IT MAY BE INVOLVED IN A MORE GENERAL CELLULAR
PROCESS SUCH AS RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 LLLTVWNFGAVGMYCIHWKGPLVLQQAYLIMISALMALVFIKYLPEWSAWYLLGAISVYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGG-LAYING-DEFECTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.1%; Score 983; DB 1; Length 461;
49.1%; Pred. No. 7.3e-61;
Live 60; Mismatches 92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92; Indels
                                                                                     LEVITAN D., GREENWALD I.; "Facilitation of lin-12-mediated signalling by sel-12, caenorhabditis elegans S182 Alzheimer's disease gene."; Nature 377:351-354(1995).
                                                                                                                                                                                                                                              INFLUENCE LIN-12 ACTIVITY INDIRECTLY.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE PRESENILIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABD50D85 CRC32;
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POTENTIAL.
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60 C
51817 MW;
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           Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   461 AA;
                                                     SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                           MEDLINE; 96032531
                                                                                                                                                                                                                                                                                                                                                                                                                  46
102
131
131
164
190
213
251
385
60
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TRANSMEM
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MUTAGEN
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=BRISTOL N2;
MEDILINE; 98004548.

LI X., GRENWALD I.;
"HOP-1, a Caenorhabditis elegans presentlin, appears to be functionally redundant with SEL-12 presentlin and to facilitate LIN-12
                                                                                                                                           83 YGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPF----TEDTPSVGQRLLNS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BRISTOL N2;
CONNELL M., MAGGI L.;
Submitted (UNN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY FACILITATE LIN-12 AND GLP-1 MEDIATED RECEPTION OF
-!- FUNCTION: MAY FACILITATE LIN-12 AND GLP-1 MEDIATED RECEPTION OF
-!- SUBCELLULAR SIGNALS.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE PRESENILIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
---LTGYPGEELE----
                                                        EPTSSDSNTSTAFPGEASCSSETPKRPKVKRIPQKVQIESNTTASTTQNSGVRVERELAA
                                                                                                                ------EEEERGVKLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and GLP-1 signaling.";
Proc. Natl. Acad. Sci. U.S.A. 94:12204-12209(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.5%; Score 524.5; DB 1 30.5%; Pred. No. 2.1e-29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
INTEGRAL MEMBRANE PROTEIN HOP-1.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                 358 AA
                                                                                                                                                                                                                              401 LTLLLLAVFKKALPALPISITFGLIFYFSTDN 432
                                                                                                                                                                                                                                                              POTENTIAL. POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39864 MW:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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107
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034430 echimys did 080739 arabidopsis 234039 echimys did 037099 echimys did 09xnm7 microtus lo 034973 microureus d 035076 marmota cau 085080 arthrobacte 034425 echimys did 034427 echimys did 034424 echimys did 034457 mus musculu 074710 emericella 09xp78 sminthopsis 09xp88 sminthopsis 09xp88 sminthopsis 035518 philander m

7.

26 104 4.5 379 8 Q34430 Q80739 COR0739 arabidops: displayed; displa	ALIGNMENTS	RESULT 1 199XT96 AC 09XT96 AC 09XT96; DT 01-NOV-1999 (TERMELRE1. 12, Last sequence update) DT 01-NOV-1999 (TERMELRE1. 12, Last sequence update) DT 01-NOV-1999 (TERMELRE1. 12, Last annotation update) DE PRESENILIN 2. OC BUARTYCATS, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; CC BOVINGE; BOS. RN [1]	SISSUE-BRAIN, SAHARA N., SHIRASAWA T., MORI H.; SAHARA N., SHIRASAWA T., MORI H.; "Molecular cloning of bovine presentlin 2 Submitted (DEC-1997) to the EMBL/GenBank/ EMBL; AF038937; AAD39024.1; SEQUENCE 449 AA; 50301 MW; A3DA878F C.	Query Match 96,9%; Score 2262.5; DB 6; Length 449; Best Local Similarity 97.1%; Pred. No. 4.7e-16; 1; Gaps Matches 436; Conservative 5; Mismatches 1; Gaps Qy 1 MLTFMASDSEEEVCDERTSLMSAESPTPRSCOERGCROCREDGENTAQMRSQENEED-GEED 59 60 PDRYCSGVPGRPPGLEEELLEKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGOL 119 Qy 60 PDRYVCSGVPGRPPGLEEELLEKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGOL 120 120 Db 120 IYTPFTEDTPSVGGRLNSVLNTLIMISVIVVMTFLVVLYKYRCYKFIHGWLIMSSLML 180 179 Qy 120 IYTPFTEDTPSVGGRLNSVLNTLIMISVLYTWTTFLVVLYKYRCYKFIHGWLIMSSLML 180 199 Qy 121 IYTPFSEDTPSVGGRLNSVLNTLIMISVLYTWTFLVVLYKYRCYKFIHGWLIMSSLML 180 299 Qy 180 LFLFTXIYLGEVLKTYNVAMDYPTLLITVWNFGAVGMVCIHWKGPLVLQQAYLIMISALM 240 Qy 241 ALVFIKXLPEWSAWVILGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMV 299 Qy 300 WITVGMAKLDPSSQGALQLPPRMEEDSYDSFGEPSYPEVFPPPLTGYPGEELEEEERRG 359 Qy 300 WITVGMAKLDPSSQGALQLPPRMEEDSYDSFGEPSYPEVFPPPLTGYPGEELEEEERRG 359
rotein - prot Dn: M Est score: 2 Ence: 1 Eng table: B Ched: 2	g g	1: sp_archea:* 2: sp_bacteria:* 3: sp_fungi:* 4: sp_human:* 5: sp_invertebrate:* 6: sp_mammal:* 7: sp_mhc:* 8: sp_organelle:* 9: sp_phage:* 10: sp_plage:* 11: sp_rodent:* 12: sp_virus:* 13: sp_virus:* 14: sp_unclassified:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES Result No. Score Match Length DB ID Description	1 2262.5 96.9 449 6 09XT96 09xt97

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117 NORDDGSVLATEAEAAGFTQEWSANLSERVARRQIEVQSTQSGNAQRSNEYRTVTAPDQN 176
                                                                                                                                                                             128 TPSVGQRLLNSVLNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----LEEELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFTED 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 ESPTPRSCQEGRQGPEDGENTAQWRSQENEEDGEEDPDRYVCSGVP----GRPPG---- 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

POWELL C.S., GEGG M.E., PALMER M.S.;

"Human presentlin I gene encodes an alternative protein-minilin.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ008005; CAA07825.1;

SEQUENCE 184 AA; 21073 MW; 5C6FBAEE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 VVEQDEEEDEELILKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTED
             300 WTV------GMAKLDPSS-----QGALQLPYDPEMEEDSYDSFGEPSYPE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 ELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRR-SLGHPEPLSNGRPQGNSRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia;
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Pred. No. 6.2e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                        KALPALPISITFGLIFYFSTDNLVRPFMDTLASHQLYI 448
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                                                                                                                    -----VFEPPLTGYPGE---ELEE-------
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                                                                                                                                                                                                                                                                                                                                                184
                                                                                                                                                                                                                                                                                                                                                                          Created)
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56.0%;
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10,
12,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              019737; 022692;
01-NOV-1996 (TrEMBLrel. 0:
01-MAY-1999 (TrEMBLrel. 1:
01-NOV-1999 (TrEMBLrel. 1:
F22E10.5 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 102; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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01-MAY-1999 (
01-MAY-1999 (
MINILIN.
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8
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                                                                                                                                                                                                                                                                                  241 APTAQPEDDGGFTPAWVNQQQHQLGPWGSTEDSRREIQELPSARPP--PVEDDEERGVKL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 VIVVMTIFLVVLXKKKCKKFIHGWLIMSSLMLLFLTXIXLGEVLKTYNVAMDYPTLLT 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLTLLLLAVFKKALPALPISITF 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                        89 IMLEVPVTLCMIVVVATIKSVRFYTEKNG-QLIYTPFTEDTPSVGQRLLNSVLNTLIMIS 147
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CANTON S;
MEDLINE; 98331525.
MARFANY G., DEL-FAVERO J., VALERO R., DE JONGHE C., WOODROW S.,
HENDRIKS L., VAN BROECKHOVEN C., GONZALEZ-DUARTE R.;
"Identification of a Drosophila presentlin homologue: evidence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75;
       SEQUENCE FROM N.A.
ARCHER S., HIRANO J., DISS J.K., FRASER S.P., DJAMGOZ M.B.A.;
Neurospeort 0.0-0(0).
EMBL; Y17128; CAA76641.1; -.
PFAM; PF01080; Presenilin; 1.
NON_TER
                                                                                                                                                Length 384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 272;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
Drosophila (FRAGMENT).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.7%; Score 576.5; DB 5;
47.8%; Pred. No. 5.7e-36;
tive 29; Mismatches 41;
                                                                                                                                             58.0%; Score 1355; DB 13;
69.9%; Pred. No. 3.9e-94;
ive 33; Mismatches 55;
                                                                                                   21A78D17 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 606B9A5C CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      423 GLIFYFSTDNLVRPFMDTLASHQLYI 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA; 29456 MW;
                                                                                                 384 AA; 43276 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alternatively spliced forms."
J. Neurogenet. 12:41-54(1998)
EMBL; AF017025; AAD01611.1;
NON_TER
                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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133; Conserv
                                                                                                                                                              Similarity
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                                                                                                                                             Query Match
Best Local Simil
Matches 270;
                                                                                  NON_TER
SEQUENCE
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Best Local Si
Matches 133;
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FGAVGMVCIHWKGPLVLQQAYLIMISALMALVFIKYLPEWSAWVILGAISVYDLVAVLCP 270
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01-AUG-1998 (TYEMBLIEL: 07, Last sequence update)
01-NOV-1999 (TYEMBLIEL: 12, Last annotation update)
RAT SKELETAL MUSCLE TYPE I VOLTAGE-GATED SODIUM CHANNEL
(RSKM1) VARIANT (RSKM1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.7%; Score 109; DB 11;
20.3%; Pred. No. 5.4;
ative 63; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ionic channel.
SEQUENCE 1840 AA; 208823 MW; 1948BOC2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1840
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314 SMMFRPISQT---LFWILTANLI 333
                                                                                                                                                                                                                                                                          412 ALPALPISITFGLIFYFSTDNLV 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00170; NACHANNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
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Best Local Similarity
Lac 98; Conserve
                                   IG-----
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070611
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-!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
BOUND TO THE PROTIEN (BY SIMILARITY).
EMBL: M99462; AAB61692.1;
PFAM; PF00033; cytochrome_b_N; 1.
Mitochondrion; Electron transport; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                             417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 93096825.
KRAJEWSKI C., DRISKELL A.C., BAVERSTOCK P.R., BRAUN M.J.;
"Phylogenetic relationships of the thylacine (Mammalla: Thylacinidae)
among dasyuroid marsupials: evidence from cytochrome b DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 VVLYKYRCYKFIHGWLIM-----SSLMLLFLFTYIYLGEVLKTYNVAMDYPTLLTTVWN 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213 AVGMVCIHWKGPLVLQQAYLIMISALMALVFIKYLPEWSAWVILGAISVYDLVAVLCPKG 272
                                                                                                                                                                                                                                                                                           --LPYDPEMEEDSYDSFG------EPSY---PEVFEP--PLTGYPGEELEEEE 357
                                                                                                                                                                                                                                                                                                                                                                                LCMIVVVATIKSVRFYTEKNGQLIYTPFTEDTPSVGQRLLNSVLNTLIMISVIVVMTIFL 156
               LCMIVVVATIKSVRFYTEKNGQLIYTPFTEDTPSVGQRLLNSVLNTLIMISVIVVMTIFL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 MCLIIQILT-----LTAFT 64
                                                                                                        --QTLVEWAWGGFSVDNPTLTRFFALHFLLPFMIAGLTIVHLTFLHETGSNNPLGLOSNC
                                                                                  157 VVLYKYRCYKFIHGWLI----MSSLMLLFLFTYIYLGEVLKTYNVAMDYPTLLLTVWNFG
                                                                                                                                                                                                                       273 PLRMLVETAQ---ERNEP----IFPALIYSSAMVWTVGMAKLDPSSQGALQ---
                                                                                                                                                                                                                                                                                                                                                           RGVKLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLTLLLLAVFKKALPALP
                                                 LCLITQIVI------GLLLAMHYTADT-------TLAFSSV----
                                                                                                                                                                                                                                                                                                                           184 DKISFHPYFSLKDLVGFTITLLLLTTLALFSPTLLGDPENFSPANPLVTTP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 8; Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequences.";
Proc. R. Soc. Lond., B, Biol. Sci. 250:19-27(1992).
-!- CATALYTIC ACTIVITY: QH(2) + 2 FERRICYTOCHROME C = Q + 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Ma
Metatheria; Dasyuromorphia; Dasyuridae; Phascolosorex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.7%; Score 110.5; DB 8;
21.1%; Pred. No. 0.7;
tive 54; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  381 AA; 42813 MW; C6A2674F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    381
                                                                                                                                                                                                                                                                                                                                                                                                                                                          288 LSQT --- LFWFLVENLF -- ILKWLGSH 309
                                                                                                                                                                                                                                                                                                                                                                                                                              ISITFGLIFYFSTDNLVRPFMDTLASH 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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les 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
CXTOCHROME B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phascolosorex dorsalis
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Q35425
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Matches
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28; 613 GIFTAEMVLKLIAMDP----YEY----FQQGWNIFDSFIVTLSLVELGLANVQGLSVL 662 564 IIYLIVMDPFVDLGITIC-IVLNTLFMAMEHY------PMTEHFDNVLSVGNLVFT 612 5 MASDSEEEVCDERTSLM-----SAESPTPRSCQEGRQGPE-DGENTAQWRSQENEE--- 55 ----- LKTYNVAMDYPTLLLTVWNFG-AVGMVCIHWKGPLVLQQAYLIMISALMAL-VFI KGPLRMLVE-----TAQERNEPIFPALIYSSAMVWTVGMAKL---DPS--SQ GALQLPYDPE-----PLTGYPGEEL EEEEEERGVKLGLGDF1F-YSVLVGKAAATGSGDWNTTLACFVA1L1GLCLTLLLLAVFKK 504 SLDASGEKGPPRPSCSADSAISDAMEELEEAHOKCPPWWYKCAHKVLIWNCCAPWVKFKH VIMLEV-----PVTLCMIVVVATIKSVRFYTEKNGQLIYTPFTE---DTPSVGQRLLN SVLNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIYLGEV-----Indels 192; Mammalia; Length 1840; ŝ

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Search completed: March 18, 2000, 22:07:43 Job time: 123 sec
  CYTOCHROME B LIGHT
                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                4.6%; Score 107; DB 8; Length 381;
ilarity 21.3%; Pred. No. 1.3;
Conservative 53; Mismatches 111; Indels 116; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILPFIVVALAIVHLLELHETGSNNPSGINPDSD---KIPFHPYYTIKDALGMTLLLLALL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 FLFTYIYLGEVLKTYNVAMDYPTLLLTVWNFGAVGMVCIHWKGPLVLQQAYLIMISALMA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----VILLLTVMA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              323 -MEEDSYDSFGEPSYPEVFEP--PLTGYPGEELEEEERGVKLGLGDFIF-YSVLVGKAA 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 SVLNTLIMISVIVVMTIFLVVLY------KYRCYKFIHGWLIM-----SSLMLL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 LVFIKYLPEWSAWVILGAISVYDLVAVLCPKGPLRMLVE-------TAQERNEP 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IFPALIYSSAMVWTVGM------AKLDPSSQGALQLPYDPE------- 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 SLIGACLIIQIL -- MGLFLAMHYTSDTLTAFSSVAHICRDVNHGWLIHNLHVNGASMFFM 92
                                                                                 SEQUENCE FROM N.A.
KRAJEWSKI C., PAINTER J., DRISKELL A.C., BUCKLEY L., WESTERMAN M.;
Sci. New Guinea 19:157-166(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             379 ATGSGDWNTTLACFVAILIGLCLTLLLLAVFKKALPALPISITFGLIFYFSTDNLV 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Metatheria, Dasyuromorphia, Dasyuridae, Antechinus.
                                                                                                                                                                                                                                                                                                       to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                       databases
                                                                                                                                                                               SEQUENCE OF 1-287 FROM N.A.
KRAJEWSKI C., BUCKLEY L., WOOLLEY P.A., WESTERMAN M.;
J. Mammal. Evol. 3:81-91(1996).
                                                                                                                              SEQUENCE FROM N.A.
KRAJEWSKI C., PAINTER J., BUCKLEY L., WESTERMAN M.;
J. Manmal. Evol. 2:25-35(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                 9C6998A0 CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 CLFLHMGRGIYYGSY-----LYKETWNIG-----
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                                                                                                                                                                                                                              SEQUENCE FROM N.A.
ARMSTRONG L.A., KRAJEWSKI C., WESTERMAN M.;
J. Mammal. 0:0-0(1998).
                      Antechinus naso (Antechinus habbema)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                      KRAJEWSKI C.;
Submitted (FEB-1998) to the EMBL/C
EMBL: U07576; AAC03634.1; -
PFAM; PF00032; cytochrome_b_C; 1.
PFAM; PF00033; cytochrome_b_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                381 AA; 42738 MW;
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Matches 76; Conserva
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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01-NOV-1996 (
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                                                                                                                                                                                                                                                                                             KRAJEWSKI C.,
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034340
ID 034340
AC 034340;
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18;
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BOUND TO THE PROTEIN (BY SIMILARITY).
EMBL: 014665; AAA99746.1; -.
PFAM: PF00032; cytcchrome_D_c; 1.
PFAM: PF00033; cytcchrome_D_N; 1.
Milcochondrion; Electron transport; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSQGALQLPYDP-----PLTGYPG 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 VVLYKYRCYKFIHGWLIM-----SSLMLLFLFTYIYLGEVLKTYNVAMDYPTLLLTVWN 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SV--AHICRDVNYGWLIRNIHANGASMFFWCLFLHVGRGIYYGSY------LYKETWN 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 IG-------VILLLIVMATAFVGYVLPWGQMSFWGATVITNLLSAIPY 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 IG--NTLVEWIWGGFSVDKATLTRFFAFHFILPFIILAMVVVHLLFLHETGSNNPTGLDP 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitochondrion.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Metatheria; Didelphimorphia; Didelphidae; Didelphis.
                                                                                                                                                                                                                                                                                                                                          PATTON J.L., REIS MARIA S.F., DA SILVA N.F.;
J. Mammal. Evol. 3:3-29(1996).
-!- CATALYTIC ACTIVITY: QH(2) + 2 FERRICYTOCHROME C = Q + 2
FERROCYTOCHROME C. - Q + 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    382 AA; 43139 MW; 907FBCA3 CRC32;
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Matches 79; Conservative
Didelphis marsuplalis
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=> e
                   PRESENILIN-2 PS2S (MOUSE PS-2SHORT ISOFORM)/CN
F.6
             1
E7
                   PRESENILIN-ASSOCIATED PROTEIN 1 (HPAP-1) (HUMAN INCYTE
CLONE
                    1353337)/CN
                   PRESENILINASE/CN
E8
             1
                   PRESEP-AGRI/CN
E9
             1
                   PRESER ACE/CN
E10
             1
                   PRESERCAR/CN
E11
             1
                   PRESERIN M 72/CN
E12
             1
                   PRESERIN T 72/CN
E13
             1
E14
             1
                   PRESERT/CN
                   PRESERVAC WETPROOF/CN
E15
E16
                   PRESERVAL/CN
E17
                   PRESERVAL B/CN
=> s e4-6
             1 "PRESENILIN-2 (HUMAN ISOFORM)"/CN
             1 "PRESENILIN-2 PS2CCAS (MOUSE)"/CN
             1 "PRESENILIN-2 PS2S (MOUSE PS-2SHORT ISOFORM)"/CN
             3 ("PRESENILIN-2 (HUMAN ISOFORM)"/CN OR "PRESENILIN-2 PS2CCAS
L1
                (MOUSE) "/CN OR "PRESENILIN-2 PS2S (MOUSE PS-2SHORT
ISOFORM) "/CN)
=> d 1-3 ide can
     ANSWER 1 OF 3 REGISTRY COPYRIGHT 2000 ACS
L1
     251358-30-2 REGISTRY
RN
     Presenilin-2 (human isoform) (9CI) (CA INDEX NAME)
CN
OTHER NAMES:
     5: PN: WO9960122 SEQID: 5 claimed protein
CN
     PROTEIN SEQUENCE
FS
MF
     Unspecified
CI
     MAN
SR
     CA
LC
     STN Files:
                  CA, CAPLUS
*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
*** USE 'SOD' OR 'SOIDE' FORMATS TO DISPLAY SEQUENCE ***
               1 REFERENCES IN FILE CA (1967 TO DATE)
               1 REFERENCES IN FILE CAPLUS (1967 TO DATE)
REFERENCE
            1: 132:11416
     ANSWER 2 OF 3 REGISTRY COPYRIGHT 2000 ACS
T.1
     200445-64-3 REGISTRY
RN
CN
     330-448-presenilin-2 (Mus musculus isoform PS2Ccas) (9CI) (CA INDEX
NAME)
OTHER NAMES:
CN
     Presenilin-2 PS2Ccas (mouse)
     PROTEIN SEQUENCE
FS
MF
     Unspecified
CI
     MAN
SR
     CA
LC
     STN Files:
                  CA, CAPLUS
*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
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